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MPsrch_pp protein - protein database search, using Smith-Waterman algorit

Tabular output not generated. Run on: Sat Nov 27 15:32:58 1999; MasPar time 23.10 Seconds 903.795 Million cell updates/se

Sequence: Description: Perfect Score:

Title:

Scoring table: PAM 150 Gap 11

Post-processing: Minimum Match 0% Listing first 45 summaries

122810 seqs, 40068593 residues

Searched:

Database:

pir60
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 52.382; Variance 142.723; scale 0.367

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

																							Res
23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	æ	7	σ	u	4	ω	N	1	Result
112	112	117	116	118	116	118	119	119	120	121	120	120	120	123	124	123	123	127	168	1100	2192	2245	Score
3.2	3.2	3.3	ω. ω	3.3	ω ω	ω. ω	3.4	3.4	3.4	3.4	3.4		3.4		ω		3.5			31.0	61.8	63.3	Query Match Length
290	187	1302	650	410	373	264	2578	2529	925	411	333	290	220	2076	857	489	168	1116	168	170	326	326	1
2	N	2	2	2	N	2	N	N	2	2	<u>, .</u>	N	2	Ν	N	ν	2	2	N	N	N	2	DB
D71921	G70406	JC6009	S14181	I38502	S76273	S34121	A56922	A56923	T01384	I58156	KIBYRB	н64591	S48450	S15999	S33821	S47608	A34952	S57382	158315	S13008	B37314	в33601	ID
signal peptidase I -	siroheme synthase - A	surface-located membr	DNA-directed RNA poly	7	hypothetical protein	transcription factor	transcription factor	transcription factor	hypothetical protein	Brn-3.2 - mouse	ribokinase (EC 2.7.1.	signal peptidase I -	hypothetical protein	fatty-acyl-CoA syntha	median body protein -	actin homolog YJL081c		hypothetical protein	WT1 - human	capsular antigen F1 p	regulatory protein Lc	lcrV protein - Yersin	Description
6.31e+00	6.31e+00	2.17e+00	2.69e+00	1.74e+00	2.69e+00	1.74e+00	1.40e+00	1.40e+00	1.12e+00	9.01e-01	1.12e+00	1.12e+00	1.12e+00	5.77e-01	4.61e-01	5.77e-01	5.77e-01	2.34e-01	9.77e-06	1.52e-139	0.00e+00	0.00e+00	Pred. No.

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RESULT		45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
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		3.0	3.0	3.0	3.0	3.1	3.1	3 .1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1				3.2	
		1325	1127	729	455	1175	1109	1004	982	973	835	835	775	711	558	416	. 311	217	1273	812	733	535	417
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		ydek protein - Escher	hypothetical protein	kinesin-related prote	nucleobindin precurso	hypothetical protein	surface-array protein	outer cell wall prote	protein pl15 homolog	coatomer complex beta	invasin - Yersinia en	invasin - Yersinia en	phage infection prote	phosphate acetyltrans	recN protein homolog	hypothetical protein	gamma-giardin - Giard	-	hypothetical protein	NIP1 protein - yeast	stringent response pr	ribosomal protein S01	hypothetical protein
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Db 301 AIEALNRFIQKYDSVMQRLLDDTSGK 326 	Db 241 GSENKRTGALGNLKNSYSYNKDNNELSHFATTCSDKSRPLNDLVSQKTTQLSDITSRFNS	Db 181 SGTINIHDKSINLMDKNLYGYTDEEIFKASAEYKILEKMPQTTIQVDGSEKKIVSIKDFL 	Db 121 VMHFSLTADRIDDDVLKVIVDSMNHHGDARSKLREELAELTAELKIYSVIQAEINKHLSS 	Db 61 NRVITDDIELLKKILAYFLPEDAILKGGHYDNQLQNGIKRVKEFLESSPNTQWELRAFMA	Db 1 MIRAYEQNPQHFIEDLEKVRVEQLTGHGSSVLEELVQLVKDKNIDISIKYDPRKDSEVFA	Query Match 63.3%; Score 2245; DB 2; Length 326; Best Local Similarity 99.4%; Pred. No. 0.00e+00; Matches 324; Conservative 2; Mismatches 0; Indels 0;	Yersinia pestisreferences MUID:90008806 sion B33601 tatus preliminary olecule_type DNA esidues 1-326 ##label PRI ross-references GB:M26405 #length 326 #molecular-weight 37226	REFERENCE A33601 #authors Price, S.B.; Leung, K.Y.; Barve, S.S.; Straley, S.C. #journal J. Bacteriol. (1989) 171:5646-5653 #title Molecular analysis of lcrGVH, the V antigen operon of	B33601 #type complete lcrv protein - Yersinia pestis #formal_name Yersinia pestis 17-Jan-1990 #sequence_revision 17-Jan-1990 23-Mar-1993 S B33601
	LSDITSRENS 300 LSDITSRENS 495	KKIVSIKDFL 240 KKIVSIKDFL 435	QAEINKHLSS 180 	TQWELRAFMA 120 TQWELRAFMA 315	DPRKDSEVFA 60 DPRKDSEVFA 255	26;	ksum 6238	ley, S.C.	#text_change

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                                                             #journal FEBS Lett. (1990) 277:230-232 #title Nucleotide sequence of the Yersinia pantigen and the primary structure of T and B cell epitopes.
#cross-references MUID:91099503 #Accession S13008
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##cross-references GB:M57893; NID:g155456; PID:g155458
# #length 326 #molecular-weight 37336 #chec
                ##cross-references
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                                             ##mg__cule_type DNA
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Local Similarity 96.6%;
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Macellaro, A.; Baeckman, A.; Boelin, I.; Wolf-Watz, H.
J. Bacteriol, (1991) 173:1607-1616
Analysis of the V antigen lcrGVH-yopbB operon of Yersinia
pseudotuberculosis: evidence for a regulatory role of LcrH
                                                                                                                                                                                                                                      Galyov, E.E.; Smirnov, O.Y.; Karlishev, A.V.;
Denesyuk, A.I.; Nazimov, I.V.; Rubtsov, K.S
V.M.; Dalvadyanz, S.M.; Zav'yalov, V.P.
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regulatory protein LcrV - Yersinia pseudotuberculosis
#formal_name Yersinia pseudotuberculosis
30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change
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> DNA
               1-170 ##labe1 G?
ces EMBL:X61996;
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Pred. No. 0.00e+00;
7; Mismatches 4
GAL
6; NID:g48620; PID:g48621
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                                                                                                            pestis gene encoding F1 of the protein. Putative
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22-170
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#map_position 11p13-11p13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##status preliminary; translated from GB/EMBL/D ##molecule_type mRNA ##residues 1-168 ##label RES ##cross-references GB:S75264; NID:g896246; PID:g896247
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Similarity 66.78;
20; Conservation
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170; Conservative
                                                                                                      hypothetical protein 00944

#formal_name Saccharomyces cerevisiae
28-0ct-1995 #sequence_revision 03-Nov-
12-pec-1997.
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I58315
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Yeast (1995) 11:975-986
A 29.425 kb segment on the
contains more than twice
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I58315
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                                                            Zumstein, E.; Pearson, B.M.;
                                                                             S57382; S66781;
S57374
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#product capsular antigen Fl #status predicted #label
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7; 1
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Pred. No. 1.52e-139;
Vismatches 0;
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Pred. No. 9.77e-06;
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              the left arm of yeast chromosome XV
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Best Local Similarity 47.1%;
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                                                                                                                                                                                                                                                                                                                                             #authors Jalajakumari, M.B.; Thomas, C.J.; Halter, R.; Manning, P.A.
#journal Mol. Microbiol. (1989) 3:1685-1695
#title Genes for biosynthesis and assembly of CS3 pili of CFA/II
enterotoxjenic Escherichia coli: novel regulation of pilus
production by bypassing an amber codon.
#cross-references MUID:90158116
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#cross-references MUID:96021609
#accession S57382
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MIPS:YOL087c
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##cross-references EMBL:X83121; NID:g600461; PID:g600471
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##residues 23-52 ##label JA2
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CS3 fimbrial protein precursor -
CS3 pilin
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Infect. Immun. (1988) 56:3297-3300
Nucleotide sequence of the gene encoding the major subunit
CS3 fimbriae of enterotoxigenic Escherichia coli.
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#product CS3 fimbrial protein
#label MAT
#length 168 #molecular-weight 1746
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07-Sep-1990 #sequence_revision
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15-29 ##label JA3
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Best Local Similarity 23.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors Miosga, T.; Schaaff-Gerstenschlaeger, I.; Chalwatzis, N.;
Baur, A.; Boles, E.; Fournier, C.; Schmitt, S.; Velten, C.;
Wilhelm, N.; Zimmermann, F.K.

#journal Yeast (1995) 11:681-689

#title Sequence analysis of a 33.1 kb fragment from the left arm of Saccharomyces cerevisiae chromosome X, including putative proteins with leucine zippers, a fungal Zn(II)(2)-Cys(6) binuclear cluster domain and a putative alpha-2-SCB-alpha-2 binding site.

#cross-references MUID:96093911
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                                                                          Similarity
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actin homolog YJL081c - yeast (Saccharomyces cerevisiae)
protein J1012; protein YJL081c
#formal_name Saccharomyces cerevisiae
11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change
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larity 25.8%;
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Pred. No. 5.77e-01;
                                                        Score 123; DB 2;
Pred. No. 5.77e-01;
21; Mismatches 24
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#title Sequence and structure of a new coiled coil protein microtubule bundle in Giardia.
#cross-references MUID:93287123
#accession S33821
##status
                                                                                                                                                                                                                 #journal #title
                                                                                                                                           longer than previously #cross-references MUID:91238709 #accession $15999
                                                                                                                                                                                                                                                                       #authors
                                                     #gene
                                                                                      ##molecule_type DNA
##residues 1-2076 ##label M
##cross-references EMBL:X59690;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##residues 1-857 ##label MAR
##cross-references EMBL:X64517; NID:g312670; PID:g312671
# #length 857 #molecular-weight 100583 #check
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   374 SSSGTINIHDKSINLMDKNLYG-YTD-EEIFKAS 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205 QHFIED-LEKVRVEQLTGHGSSVLEELVQLVKDKNIDISIKYDPRKDSEVFA-NRVITD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 3.5%;
Local Similarity 20.1%;
nes 43; Conservative
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median body protein - Giardia lamblia
#formal_name Giardia lamblia
06-Jan-1995 #sequence_revision 06-Jan-1995
09-Sep-1997
                                                                                                                                                                                                                                                                                                                     #formal_name Yarrowia lipolytica, Candida lipolytica
30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
13.Sep-1998
#length 2076 #m
                                                                                                                                                                         The pentafunctional FAS1 genes of Saccharomyces cerevisiae and Yarrowia lipolytica are co-linear and considerably longer than previously estimated.
                                 *superfamily yeast fatty-acyl-CoA synthase beta chain
                                                                                                                                                                                                                                Mol. Gen. Genet. (1991) 226:310-314
                                                                                                                                                                                                                                                                       Koettig,
                                                                                                                                                                                                                                                                                                                                                                        fatty-acyl-CoA synthase (EC (Yarrowia lipolytica)
                                                                                                                                                                                                                                                  Schweizer, E
                                                                                                                                                                                                                                                                   H.; Rottner, G.;
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#molecular-weight 230223
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Pred. No. 4.61e-01;
71; Mismatches 82
                                                                               MOL
; NID:g297854; PID:g297855
                                                                                                                                                                                                                                                                   Beck, K.F.;
                                                                                                                                                                                                                                                                                                                                                                                         2.3.1.86) beta chain - yeast
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Best Local Similarity 22.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1268 TDRNTRIKEFYWKLWFGQDSK-FEIDTDIT-EEIIGDDVTISGKAIADFVHAVGNKGEAF 1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type DNA
##residues 1-220 ##label
##cross-references GB:247047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 DDKLISIGNVHAANHSKLQNIQMVVMKNE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 AAGKYTDAVTVTVSNQEFMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLLQRSHVLLNQHFDNMNVKSNQDARRN-NDDQAIQYTIPFAFISEVVPGSPSDKADIKV 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVRVE-QLTGHGSSVLEELVQLVKDKNIDISIKYDPRKDSEVFANRVITDDIELLKKILA 271
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Similarity 31.3%;
25; Conservative
                                    Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.;
Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk,
H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush,
J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.;
Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.;
McKenney, K.; Fitzegerald, L.M.; Lee, N. Jadams, M.D.;
Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback, T.R.;
Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.;
Fujii, C.; Bowman, C.; Watthey, L.; Wallin, E.; Hayes,
W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
C.M.; Venter, J.C.
Nature (1997) 388.539-947
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#length 220 #molecular-weight 24846 #checksum
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02-Dec-1994 #sequence_revision 02-Dec
12-Dec-1997
The complete genome sequence Helicobacter pylori.
                                                                                                                                                                                                                                                                                                H64591
A64520
                                                                                                                                                                                                                                                                                                                                        H64591 #type complete
signal peptidase I - Helicobacter pylori (strain 26695)
#formal_name Helicobacter pylori
09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change
10-Oct-1997
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Pred. No. 1.12e+00;
39; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 123; DB 2;
Pred. No. 5.77e-01;
22; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL Data Library, August 1994
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                       of the
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#accession S12918
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                                                                                                                                                                                                                                                                                                                                                                   cession ...
##molecule_type DNA
##residues 1-333 ##label DUJ
##cross-references EMBL:x59720; NID:g1907116; PID:e264378;
##Cross-references EMBL:X59720; NID:g1907116; PID:e264378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 VGDDVVLATGSQDFFVRSIGSKGGKLAAGK-YTDAVTVTVSNQEFMIRAY-EQNPQ-HFI 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 IGGDEVLFT-NEGFYLHPFESDTDKNYIAKHYPNAMTKEFMGKIFVLNPYKNEHPGIHYQ 169
                                                                                                                                       176 KLAAGKYTDAVTVTVSNQEFMIRAYEQNPQHFIEDLEKVRVEQLTGHGSSVLEELV-QLV
                                                                                                                                                          235 KLMNRKKRGIVVMTLGSRGVLFCSHESPEVQFLPAIQNVSVVDTTGAGDTFLGGLVTQLY 294
                                                                                                                                                                                                                                                                                                                                                  ##cross-references SGD:S0000632; MIPS:YCR036w
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NCE S19445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##molecule_type DNA ##label THI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 KDNETFHLMEQLATQGAEANISMQLIQMEGEK 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##cross-references GB:AE000571; GB:AE000511; NID:g2313686; PID:g2313695; TIGR:HP0576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##status
                                                                    235 KDKNIDISIKYDPRKDSEVFANRVITDDIELLKKI 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 EDLEKVR-VEQLTGHGSSV-LE-ELVQLVKDK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type DNA
                                                                                                                                                                                                           y Match 3.4%;
Local Similarity 23.2%;
nes 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 3.4%;
Local Similarity 27.2%;
nes 25; Conservative
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                                                                                                     QGETLSMAIKFSTLASSLTIQRKGAAESMPLYKDV 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KIBYRB #type complete ribokinase (EC 2.7.1.15) - yeast (Saccharomyces cerevisiae) protein YCR036w; protein YCR523 #formal_name Saccharomyces cerevisiae 31.Mar-1993 #sequence_revision 31.Mar-1993 #text_change 12-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nces MUID:97394467
H64591
                                                                                                                                                                                                                                                                          #superfamily ribokinase
phosphotransferase
#length 333 #molecular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the Protein S19448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The complete sequence of the 8.2 kb segment left chromosome III reveals five ORFs, including a great ribokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     $12918; $19448
$12916; $19448
Thierry, A.; Fairhead, C.; Dujon,
Yeast (1990) 6:521-534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herbert, C.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #length 290
   I58156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation not shown
#type
                                                                                                                                                                                                                                                                              #molecular-weight 36984 #checksum 5645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jia, Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 120; DB 2; Le
Pred. No. 1.12e+00;
28; Mismatches 32;
                                                                                                                                                                                                           Score 120; DB 1; Lo
Pred. No. 1.12e+00;
25; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Slonimski,
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ACCESSIONS
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#authors
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ORGANISM
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                                     Matches
                                                    Best Local
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Best Local :
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348-404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 НИНИНИНИНИРРИQALEGELLEHLSPGLALGAMAGPDGTVVSTPAHAPHMATMNPMHQA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##status preliminary; translated from GB/EMBL/DDBJ ##molecule_type mRNA #molecule_type mRNA ##residues 1-411 ##label RES ##cross-references GB:S68377; NID:g545068; PID:g545069
                                                                                                                                                                                                                               ##cross-references EMBL:AF069442; NID:g3242970;
                                                                                                                                                                                                                                                 ##molecule_type DNA
##residues 1-925 ##label PAR
565 RHAESLIPSSLNEEDFLLLRVFCDQLQPLIHSEFEESQVQDIEGRGGNLSGKLKELLNLN 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 ALSMAHAHGLP-SHMGCMSDVDAD 256
                                                                                                                                                                                                                                                                                         ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 RITLTYKEGAPITIMD-NGNIDTE
                                                                                                                                                                                                                   #experimental_source cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 HHHHHHHHHHSSGHIDDDDKHMKKISSVIAI-ALFGTIATANAADLTASTTATATLVEPA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14
                                 h 3.4%;
Similarity 17.4%;
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.4%;
Similarity 28.6%;
                                                                                                                       4
10/3; 54/3; 96/3; 148/3; 176/3; 219/3; 292,
418/3; 515/1; 561/1; 584/2; 604/3; 761/3
                                                                                                                                                                                                                                                                                                                         Parnell, L.D.; Gnoj, L.; de la Bastide, Habermann, K.; Schutz, K.; Huang, E.; Dedhia, N.N.; McCombie, W.R. submitted to the EMBL Data Library, May Genomic sequence of BAC T419 from Arabic chromosome IV, near 16.6 cM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Turner, E.E.; Jenne, K.J.; Rosenfeld, Neuron (1994) 12:205-218
Brn-3.2: a Brn-3-related transcription distinctive central nervous system exegulation by retinoic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T01384 #type complete
hypothetical protein T419.3 - Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mou
                                                                                                                                                                                                                                                                                                          T01384
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#length 411
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26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
__17_Oct-1997
                                                                                                       #length 925 #molecular-weight 102857 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                     Z14314
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                               Score 120; DB 2; Le
Pred. No. 1.12e+00;
43; Mismatches 29;
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Pred. No. 9.01e-01;
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                                                                                                                                                               292/3; 336/3; 367/3;
                                                                                                                                                                                                                                                                                                                                                                1998
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Gottesman, 1
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ENTRY
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Search completed: Sat Nov 27 15:34:00 1999 Job time : 62 secs.
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                                                                                                                                                                                                                                                                                                           Query Match 3.4%;
Best Local Similarity 24.6%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            schnurri is required for Drosophila Dpp signaling and encodes a zinc finger protein similar to the mammalian transcription factor PRDII-BF1.

#cross-references MUID:95292346
#accession A56923
##Status
                                                                                                                                                                                                                                                                                                                                                                                                                                              #gene
                                                                             158
                                                                                                                                                                                                                                                                                                                                                                                     ane FlyBase:shn

##cross-references FlyBase:FBgn0003396

RDS DNA binding; transcription factor; zinc finger

RDS #length 2529 #molecular-weight 271637 #checksum 9689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type mRNA
#residues 1-2529 ##label GRI
##cross-references GB:L42311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               625 NEEASEDCDVRVEG-VMTKQGVNEEIDTVERL 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 KYTDA-VTVTVSNQEFMI-RAYEQNPQHFIE-DLEKVRVEQLTGHGSSVLEELVQLVKDK 237
                                                                                                                 145 LPTVDSNHII 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 NIDISIKYDPRKDSEVFANRVITDDIELLKKI 269
                                                                                                                                                                                           89
                                                                                                                                                         86
                                                                                                                                                                                                                                 : |:| || :|:||: | |:: ||:| ||: || : : : ::::|:: 38 TIATANAADLTASTTATATLVEPARITLTYKEGAPITIMDNGNIDTELLVGTLTLGGYKT 97
                                                                                                                                                                                                                                                                   30 ATAAAAAAAAATTTVTTAATPTKKR-TYRETATATTVTQRSTNKANIAAAIALAAATE 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
                                                                                                                                             STISTSVNFTDAAGDPMYLTFTSQDGNNHQFTTKVIGKDSRDFDISPKVNGENLVGDDVV 157
                                                                                                                                                                           ATASASASATATATDAT-LT-ASKAAATAAATTDAASGNSNSSSKPSTSTRDKL-GE-VP 144
                                                                             LATGSQDFFV 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #formal_name Drosophila melanogaster
11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change
17-Mar-1999
A56923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary; nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                         Score 119; DB 2; Length 2529; Pred. No. 1.40e+00; 38; Mismatches 55; Indels 5;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Nov 27 15:34:17 1999; MasPar time 16.09 Seconds 915.415 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-08-699-716A-2 (1-521) from US08699716A.pep 3546

Sequence: 1 MGHHHHHHHHHSSGHIDDD......RFIQKYDSVMQRLLDDTSGK 521

Scoring table: PAM 150 Gap 11

Searched 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 53.725; Variance 122.928; scale 0.437

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	2245	63.3	326	- ;	LCRV_YERPE	VIRULENCE-ASSOCIATED V	0.00e+00
2	2192	61.8	326	\vdash	LCRV_YERPS	VIRULENCE-ASSOCIATED V	0.00e+00
ω	1100	ш	170	Н	CAF1_YERPE	F1 CAPSULE ANTIGEN PRE	5.16e-166
4	127	3.6	168	Ľ	FMS3_ECOLI	CS3 FIMBRIAL SUBUNIT A	3.27e-02
ъ	123	3.5	489	H	ARP4_YEAST	ACTIN-LIKE PROTEIN ARP	9.34e-02
თ	124	3.5	857	ш	MEDB_GIALA	MEDIAN BODY PROTEIN.	7.20e-02
7	123	ω .5	2076	سر	FAS1_YARLI	FATTY ACID SYNTHASE, S	9.34e-02
œ	120	3.4	220	ш	PSD9_YEAST	PROBABLE 26S PROTEASOM	2.02e-01
9	120	3.4	333	1	RBSK_YEAST	PROBABLE RIBOKINASE (E	2.02e-01
10	121	3.4	411	سا	BR3B_MOUSE	BRAIN-SPECIFIC HOMEOBO	1.56e-01
11	118	ω.ω	410	۳	BR3B_HUMAN	BRAIN-SPECIFIC HOMEOBO	3.36e-01
12	114	3. ₂	406	ш	BR11_BRARE	BRAIN-SPECIFIC HOMEOBO	9.11e-01
13	113	3.2	733	—	SPOT_MYCPN	PROBABLE GUANOSINE-3',	1.16e+00
14	115	3.2	812	ш	NIP1_YEAST	NUCLEAR TRANSPORT PROT	7.11e-01
15	109	3.1	173	۳	HA34_BRELC	HAM34 PROTEIN.	3.06e+00
16	111	3.1	311	سو	GIAG_GIALA	GIARDIN GAMMA CHAIN.	1.89e+00
17	111	3.1	467	Н	ZIC3_HUMAN	ZINC FINGER PROTEIN ZI	1.89e+00
18	110	3.1	558	Н	RECN_HAEIN	DNA REPAIR PROTEIN REC	2.41e+00
19	109	3.1	710	Н	PTA_HAEIN	PHOSPHATE ACETYLTRANSF	3.06e+00
20	109	3.1	775	\vdash	YHGE_BACSU	HYPOTHETICAL 84.1 KD P	3.06e+00
21	110	3.1	835	<u> </u>	INVA_YEREN	INVASIN.	2.41e+00
22	111	3.1	973	Н	COPB_YEAST	COATOMER BETA SUBUNIT	1.89e+00
23	109	3.1	982	سا	P115_MYCGE	P115 PROTEIN HOMOLOG.	3.06e+00

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Query Match 63.3%; Best Local Similarity 99.4%; Matches 324; Conservative

Score 2245; DB 1; Pred. No. 0.00e+00; 2; Mismatches 0

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61 NRVITDDIELLKKILAYFLPEDAILKGGHYDNQLQNGIKRVKEFLESSPNTQWELRAFMA 120

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ECDYSONE RECEPTOR (ECD	CYTOCHROME P450 CY369.	MAJOR ANTIGEN.	GOLGIN-160 (MALE-ENHAN	HYPOTHETICAL 136.5 KD	120 KD SURFACE-EXPOSED	SYNAPTONEMAL COMPLEX P	IMPORTIN BETA-1 SUBUNI	AMINOPEPTIDASE II (EC	KINESIN-LIKE PROTEIN K	CLPB PROTEIN.	KINESIN-LIKE PROTEIN K	SERINE/THREONINE PROTE	MYOSIN HEAVY CHAIN, CL	ZINC FINGER PROTEIN ZI	NUCLEOBINDIN PRECURSOR	PROBABLE PYRIDINE NUCL	CYCLIC AMP RECEPTOR 2.	HYDROGENASE EXPRESSION	HYPOTHETICAL PROTEIN B	NUCLEOCAPSID PROTEIN.	OUTER CELL WALL PROTEI
9.83e+00	9.83e+00	6.20e+00	6.20e+00	3.88e+00	6.20e+00	7.81e+00	6.20e+00		3.88e+00	7.81e+00	4.90e+00	3.88e+00	4.90e+00	4.90e+00	3.88e+00	7.81e+00	6.20e+00	6.20e+00	6.20e+00	6.20e+00	1.89e+00

ALIGNMENTS

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G155450; ALT_SEQ. 333601. SEN; VIRULENCE. AA; 37226 MW;	ntry is copyris Institute of Institute of Informatics Institution in the institution statement is a license agricultus a license is a l	171:5646-5653(19 POSSIBLY INVOLVE WHICH INCLUDES AR LOCATION: SECR	K.Y., BARVE is of lcrGVH,	ESTIS. D1. PROTEOBACTERIA; GAMMA PROM N.A.	ARD; I	
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROGGENKAMP A., HEESEMANN J;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA
-!- FUNCTION: INVOLVED IN CA(2+) REGULATION OF
INCLUDES THE EXPORT PROCESS.
                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                      EMBL; M57893; G155458; -. EMBL; X96802; E239989; -. PIR; B37314; B37314.
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BAECKMAN A., BOELIN I., WOLF-WATZ H.;
"Analysis of the V antigen lcrowl-yopBD
pseudotuberculosis: evidence for a regul
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MEDLINE; 91154114
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01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
VIRULENCE-ASSOCIATED V ANTIGEN (LOW CALCIUM R
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P23994;
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                                                                                             . Similarity 315; Conse
                                                                                                                                                                                                                                                                                                                  s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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326 AA; 37336 MW
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Matches 17
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P26948;
01-AUG-1992 (REL.
01-AUG-1992 (REL.
01-DEC-1992 (REL.
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MEDLINE; 91099503.
GALYOV E.E., SMIRNOV O.Y., KARLISHEV
DENESYUK A.I., NAZIMOV I.V., RUBTSOV
DALVADYANZ S.M., ZAV'YALOV V.P.;
                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                          FEBS
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BACTERIA; PROTEOBACTERIA;
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ELLYGTLTLGGYKTGTTSTSVNFTDAAGDPMYLTFTSQDGNNHQFTTKVIGKDSRDFDIS
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170; Conservative
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LAST SEQUENCE UI
LAST ANNOTATION
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F1 CAPSULE ANTIGEN.
CONTAINS POTENTIAL F
THAT MAY STIMULATE I
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Pred. No. 5
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                                                                                             Mismatches
                                                                                                        1100; DB 1;
No. 5.16e-166;
                                                                                                                                                                                                                                                                                                                                                                                                                  A.V.,
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ABRAMOV V
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Best Local S
Matches 4
                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Surface antigen 1, and coli surface antigen 3 fimbriae from enterotoxigenic Escherichia coli.";

J. BACTERIOL. 171:6372-6374(1989).

-i- FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5 MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JALAJAKUMARI M.B., THOMAS C.J., HALTER R., MANNING P.A.; "Genes for biosynthesis and assembly of CS3 pili of CFA/II enterotoxigenic Escherichia coli: novel regulation of pilus production by bypassing an amber codon."; MOL. MICROBIOL. 3:1685-1695(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FMS3_
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-APR-1990 (REL. 14, LAST SEGUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CS3 FIMBRIAL SUBUNIT A PRECURSOR (CS3 PILIN).
                                                                                                                                                                                                                                                                                                                          FIMBRIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Purification and analysis of colonization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 90036735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-E9034A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Nucleotide sequence of the gene encoding the fimbriae of enterotoxigenic Escherichia coli." INFECT. IMMUN. 56:3297-3300(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BOYLAN M., SMYTH C.J.,
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S07904; S07904.
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MKKISSV-IAIALFGTIA-TANAADLTASTTATATLVEPARITLTYKEGAPITIMDNGNI
                                                                                                                                                                                                                                                                                                                                                                                                  X16944; G41161; -. M35657; G145627; -
                                                                                                      h 3.6%;
Similarity 24.1%;
41; Conservative
                                                                                                                                                                                                                                                                                                                        SIGNAL.
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83
168
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                                                                                                                                                                                                               MW.
                                                                                                      Score 127; DB 1; I
Pred. No. 3.27e-02;
47; Mismatches 72;
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N -> S (IN REF. 2).
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HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence analysis of a 33.1 kb fragment from the left arm of Sacchbaromyces cerevisiae chromosome X, including putative proteins with leucine zippers, a fungal zn(II)2-Cys6 binuclear cluster domai and a putative alpha 2-SCB-alpha 2 binding site.";
YEAST 11:681-689(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARP4 OR ACT3 OR YJL081C OR J1012.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES;
                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinforthe European Bioinformatics Institute use by non-profit institutions as 1c modified and this statement is not remo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HARATA M., KARWAN A.,
"An essential gene of
related protein.";
PROC. NATL. ACAD. SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (REL. 31,
01-FEB-1995 (REL. 31,
01-NOV-1997 (REL. 35,
                                                                                                                                                                                                                        SGD; L0000027; ARP4.
PROSITE; PS01132; ACTINS_ACT_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
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X83502; G929875; -.

; Z49356; G1008244; -.

S47608; S47608.
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. ACAD.
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larity 25.8%;
Conservative
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54831 MW; C
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Saccharomyces
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LAST SEQUENCE UI
LAST ANNOTATION
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U.S.A. 91:10757-10757(1994).
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21;
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Pred. No. 9
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                                                                                                                                    C41435B1 CRC32;
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                                                   Mismatches
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Q08014;
01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
15-DEC-1998 (REL. 31, LAST)
16-DEC-1998 (REL. 31, LAST)
16-DE
                                                                                                                                                FAS1_YARLI
P34229;
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MARSHALL
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CYTOSKELETON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence and structure of a new microcubule bundle in Giardia.";
J. MOL. BIOL. 231:521-530(1993).
-!- FUNCTION: MAY HAVE A ROLE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
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MEDIAN BODY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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SUBCELLULAR LOCATION: MEDIAN BODY.
DOMAIN: SHOWS AN ALPHA-HELICAL COILED COIL STRUCTURE REPEATING HEPTADS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                          DIELLK-KILAYF-LPEDTILKGGHYDNQLQNGIKRV-K-EFLESSPNTQ-WELRA-FMA
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857 AA;
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                                                                                                                                                                     STANDARD;
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DMONADIDA; HEXAMITIDAE; GIARDIINAE; GIARDIA
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Pred. No. 7.2
71; Mismatch
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d. No. 7.20e-02;
Mismatches 82;
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CRC32;
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ACT_SITE
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                                                                                  1268
                                                                                                                                                                                                                     TRANSFERASE; HYDROLASE;
DOMAIN 1 470
DOMAIN 482 869
DOMAIN 1156 1647
                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CX161-1B;
MEDLINE; 91238709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YARROWIA LIPOLYTICA (CANDIDA LIPOLYTICA)
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN] MALONYLTRANSFERASE THIOESTERASE (EC 3.1.2.14)].
    178
                                                       119
                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3-HYDROXYPALMITOYL-[ACYL-CARRIER PROTEIN] DEHYDRATASE.

CATALYTIC ACTIVITY: ACETYL-COA + U MALONYL-COA + 2U NADPH =
LONG-CHAIN FARTY ACID + (N+1) COA + U CO(2) + 2U NADP(+).

CATALYTIC ACTIVITY: ACETYL-COA + U MALONYL-COA + 2U NADP(+).

CATALYTIC ACTIVITY: ACETYL-COA + U MALONYL-COA + 2U NADP(+).

CATALYTIC ACTIVITY: ACETYL-COA + U CO(2) + 2U NADP(+).

CATALYTIC ACTIVITY: ACETYL-COA + (ACYL-CARRIER PROTEIN] = CO
+ ACETYL-[ACYL-CARRIER PROTEIN].
                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bloinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               = 2-HEXADECENOYL [ACYL-CARRIER PROTEIN] + H(2)0.

CATALYTIC ACTIVITY: ACYL-(ACYL-CARRIER PROTEIN] + NAD(+) = DEHYDROACYL-(ACYL-CARRIER PROTEIN] + NADH.

CATALYTIC ACTIVITY: OLEOYL-[ACYL-CARRIER PROTEIN] + H(2)0 =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       + MALONYL-[ACYL-CARRIER PROTEIN]
CATALYTIC ACTIVITY: (3R)-3-HYDRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEN. GENET. 226:310-314(1991).
FUNCTION: FATTY ACID SYNTHETASE CATALYZES
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACETYLTRANSFERASE AND MALONYLTRANSFERASE, S-ACYL FA: SYNTHASE THIOESTERASE, ENOYL-[ACYL-CARRIER PROTEIN]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LONG-CHAIN FATTY ACIDS FROM ACETYL-COA, MALONYL-COA AND NADPH THE BETA SUBUNIT CONTAINS DOMAINS FOR: [ACYL-CARRIER PROTEIN]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT:
                                                                                                                                                                                                                                                                                                         SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACYL-CARRIER PROTEIN + OLEATE
                             V-GRSTSAGTV-FAPMDFAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pentafunctional FAS1 genes
                                                                                 TDRNTRIKEFYWKLWFGQDSK-FEIDTDIT-EEIIGDDVTISGKAIADFVHAVGNKGEAF 1325
  AAGKYTDAVTVTVSNQEFMI
                                                                                                                                                                                                                                                                           PF00698; Acyl_transf; ACID BIOSYNTHESIS; MUI
                                                                                                                                                                                                                                                                                                                   x59690; G297855; -.
                                                                                                                                                                                                                                                                                                                                              s requires a license agreement (Some email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNIT: FATTY ACID SYNTHETASE ARE [ALPHA(6)BETA(6)] HEXAMERS MULTIFUNCTIONAL SUBUNITS (ALPHA & BETA).
                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H., ROTTNER
                                                                                                              25;
                                                                                                                                                               482 E
1156 16
1648 18
276 2
1832 18
2076 AA;
                                                                                                                                                                                                                                                                                                       S15999
                                                                                                             Conservative
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1647
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276
1832
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                                                       IGKDSRDFDISPKVNGENLVGDDVVLATGSQDFFVRSIGSKGGKL
                                                                                                                                                                  230223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (3R)-3-HYDROXYPALMITOYL-[ACYL-CARRIER PROTEIN]
YL-CARRIER PROTEIN] + H(2)O.
                                                                                                                                                                                                                                                                              MULTIFUNCTIONAL
                             1343
                                                                                                            Pred.
22; 1
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ACETYL TRANSFERASE (
MALONYLTRANSFERASE (
MW; E10A5234 CRC32;
                                                                                                                                                                  WW.
                                                                                                                                                                                                                                   ENOYL REDUCTASE
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                                                                                                                                                                                                                                                 ; NAD; NADP.
ACETYL TRANSFERASE.
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                                                                                                                                                                                                                                                                                                                                                                                   Bioinformatics and the I
titute. There are no resi
ns as long as its content
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                                                                                                             Mismatches
                                                                                                                          123;
No. 9.
                                                                                                      DB 1;
9.34e-02;
                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                            ENZYME;
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                                                                                                                                    Length 2076;
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              01-MAY-1992
01-MAY-1992
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BARRELL B.G., BADCOCK K., BANKIER A.T., BOWMAN S., BROWN D., CHURCHER C.M., CONNOR R., COPSEY T., DES, DEVIIN K., FRASER GENTLES S., HAMLN N., HORSNELL T.S., HUNT S., JAGELS K., JONES LOUIS E., LYE G., MOULE S., MOULE T., ODELL C., PEARSON D., RAJANDREAM M.A., RILES L., ROWLEY N., SKELTON J., SMITH V., WALSH S.V., WHITEHEAD S.; SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not remove entitles requires a license agreement (so or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "cDNA cloning and characterization of a human subunit, p27 (PSMD9)."; GENOMICS 50:241-250(1998).
-!- FUNCTION: ACTS AS A REGULATORY SUBUNIT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 98317538.
WATANABE T., SAITO A., SUZUKI M., FUJIWARA T., TAKI SLAUGHTER C.A., DEMARTINO G.N., HENDIL K.B., CHUNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
STRAIN=S288C / AB
                                                       P25332;
                                                                                                                                                                                                                                                                                                                                                            PROTEASOME
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
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15-DEC-1998
  PROBABLE
                                                                   RBSK_YEAST
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P40555;
                                                                                                                          331
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1; PF00595; PDZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE PROTEASOME SUBUNIT P27 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                         ; Z38113; G558397;
; Z47047; G763339;
S48450; S48450.
; PF00595; PDZ; 1.
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                                                                                                                                                                                                         HLLQRSHVLLNQHFDNMNVKSNQDARRN-NDDQAIQYTIPFAFISEVVPGSPSDKADIKV 153
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  RIBOKINASE
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               (REL.
(REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REL. 31, CREATED)
(REL. 31, LAST SEQUENCE UPDATE)
(REL. 37, LAST AUROTATION UPDAT
PROTEASOME REGULATORY SUBUNIT
                                                                                                                                                                                                                                                                                        3.4%;
larity 22.8%;
Conservative
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                                                                    STANDARD;
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. 37, LAST ANNOTATION (
ASE (EC 2.7.1.15).
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39; N
                                                                                                                                                                                                                                                                                                      Score 120;
Pred. No. 2.
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SUBUNIT P27
                            UPDATE)
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               UPDATE)
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                                                                                                                                                                                                                                                                                                     DB 1;
.02e-01
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HUNG C.H.,
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TANAHASHI N.,
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Best Local
SEQUEL.
STRAIN=CD;
STRAINE; 94215319.
MEDLINE; 94215319.
THEIL T., ZECHNER U., KLETT
THEIL T. ZECHNER U., KLETT
                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE: 94121912.

TURNER E.E., JENNE K.J., ROSENFELD.
"BITN-3.2: a BITN-3-related transcrip
central nervous system expression at
NEURON 12:205-218(1994).
[2]
                                                                                                                                                                                                                                                                                                                                                                              BR3B_MOUSE STANDARW;

Q63934; Q63954;
Q63934; Q63954;
Q1-NOV-1997 (REL. 35, CREATED)
Q1-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
Q1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
Q1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RBK1 OR YCR036W OR YCR36W OR YCR523.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMLASCOMYCETES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
[1]
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SEQUENCE FROM N.A.
FY1679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00294; PfkB;
HSSP; P05054; 1RKD.
TRANSFERASE; KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S12918; KIBYRB.
SGD; L0001587; RBK1.
PROSITE; PS00583; PFKB_KINASES_1;
PROSITE; PS00584; PFKB_KINASES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                       POU4F2 OR BRN3B.
MUS MUSCULUS (MC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
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THIERRY A., FAIRHEAD
                                                                                                                                                                                                                                                                                                                 RODENTIA; SCIUROGNATHI;
                                                                                                                                                                                                                                                                                                                                       EUKARYOTA;
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-!- PATHWAY: FIRST STEP IN RIBOSE METABOLISM.
-!- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLAAGKYTDAVTVTVSNQEFMIRAYEQNPQHFIEDLEKVRVEQLTGHGSSVLEELV-QLV 234
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22; Conser
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larity 23.2%;
Conservative
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                         KLETT C.
tion and
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of the 8.2 kb segment
five ORFs, including
                                                                                                               N.A.
                                                                                                                                                                             ROSENFELD M.G.;
ed transcription f
expression and reg
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Pred. No. 2.02e-01,
25; Mismatches 4;
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AE; MURINAE; MUS.
                    , ADOLPH S., r
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                         MOEROEY T. the murine
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sequences

Brn-3

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Best Local S
Matches 2
                    BR3B_HUMAN STANDARD;
Q12837; Q13883; Q14987;
Q1 101.NOV-1997 (REL. 35, LAST SE
01-NOV-1997 (REL. 35, LAST SE
01-NOV-1997 (REL. 35, LAST ANI
BRAIN-SPECIFIC HOMEOBOX/POU DO
POCAFZ OR BRN3B.
HOMO SAPTENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             developmental control genes.";

CYTOGENET. CELL GENET. 66:267-271(1994).

-!- FUNCTION: MAY PLAY A ROLE IN DETERMINING OR MAINTAINING THE IDENTITIES OF A SMALL SUBSET OF VISUAL SYSTEM NEURONS.

-!- SUBCELLULAR LOCATION: NUCLEAR.

-!- TISSUE SPECIFICITY: BRAIN, PERIPHERAL SENSORY NERVOUS SYSTEM AND RETINA. IN THE ADULT NERVOUS SYSTEM BRN-3:2 PREDOMINATES IN THE OPTICAL, INTERMEDIATE, AND DEEP GRAY AREAS OF THE SUPERIOR CLLICULUS. THE DORSAL COLUMN OF THE MESENCEPHALIC AND PONTINE CENTRAL GRAY, AND THE LATERAL INTERPEDUNCULAR NUCLEUS.

-!- DEVELOPMENTAL STACE: IN THE CNS IT IS SELECTIVELY EXPRESSED IN POSTMITOTIC, TERMINALLY DIFFERENTIATED NEURONS.

-!- SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS. BELONGS
                                                                                                                                                                                                                                                                                                           DNA_BIND
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00046; homeobox; PFAM; PF00157; pou; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:102524; POU4F2,
PROSITE; PS00027; HOMEOBOX_1;
PROSITE; PS00035; POU_1; 1.
PROSITE; PS00465; POU_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This
          EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; S68377; G545069; -. EMBL; S69351; G546434; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as modified and this statement is not removed. U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between
                                                                                                                                                                                     234
                                                                                                                                                                                                                          174 HHHHHHHHHHQPHQALEGELLEHLSPGLALGAMAGPDGTVVSTPAHAPHMATMNPMHQA 233
                                                                                                                                                            62 RITLTYKEGAPITIMD-NGNIDTE 84
                                                                                                                                                                                                             w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TO CLASS-4 POU.
                                                                                                                                                                                    ALSMAHAHGLP-SHMGCMSDVDAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                            HHHHHHHHHSSGHIDDDDKHMKKISSVIAI-ALFGTIATANAADLTASTTATATLVEPA 61
                                                                                                                                                                                                                                                             h 3.4%;
Similarity 28.6%;
24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS50071;
 ; METAZOA; C
CATARRHINI;
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43
54
69
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112
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173
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1AU7.
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                                             35, CREATED)
35, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
36, TAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POU_2; 1.
HOMEOBOX_2;
                                                                                                                                                                                                                                                                                                                         51
67
77
121
131
140
184
406
98
 CHORDATA; VE
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                                                                                                                                                                                                                                                          Score 121; DB 1; L
Pred. No. 1.56e-01;
22; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                              POLY-GLY.
POLY-SER.
POLY-HIS.
POLY-HIS.
POLY-SER.
POLY-SER.
POLY-HIS.
POLY-HIS.
POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-MET.
POLY-SER.
                                                                                                                                                                                                                                                                                                           RRACLPTPP -> MCAFYLQLQ (IN RM -> KV (IN REF. 2). ; 99973657 CRC32;
           VERTEBRATA;
                                                                                                                                                                                    256
                                                                                                            410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      There are no restrictions ong as its content is in
                                                                                                            A
            MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Usage
                                               (BRN-3B).
                                                                                                                                                                                                                                                                                   Length 411;
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                     REF.
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Query Match
Best Local
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                                              DOMAIN
DNA_BIND
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CONFLICT
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DOMAIN
DOMAIN
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PFAM; PF
                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 93324388.

RING C.J.A., LATCHMAN D.S.;
The human Brn-3b POU transcription factor shows only limited outside the conserved POU
                                                                                                                                                                                                                                                          EMBL; U06233; G458391; -. EMBL; X71488; G312469; -. EMBL; L20434; G508494; -.
                                                                                                                                                                                                                                                                                            use by non-profit institutions as lon modified and this statement is not removentitles requires a license agreement (s or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins in activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homology to the Brn-3a/RDC-1 factor outside
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SEQUENCE FROM N.A.
                                      SEQUENCE
                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Jurkat T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                           BHARGAVA A.K., LI Z., WEISSMAN S.M.; "Differential expression of four mem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XIANG M., ZHOU L.-J.,
"Brn-3b: a POU domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 94000832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=RETINA
                                                                                                                                                                                                                                                                                                                                                                                            -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 146-410
                                                                                                                                                                                                                                                                                                                                                                                                C. NATL. ACAD. SCI. U.S.A. 90:10260-10264(1993).
FUNCTION: MAY PLAY A ROLE IN DETERMINING OR MAINTAINING
IDENTITIES OF A SMALL SUBSET OF VISUAL SYSTEM NEURONS.
SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: STI
TO CLASS-4 POU
                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: BRAIN. SEEMS TO BE SPECIFIC
                                                                                                                                                                                 PF00046; homeobo PF00157; pou; 1. P10037; laU7.
         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACIDS RES. 21:2946-2946(1993).
                                                                                                                                                                        PROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF 275-392
94052142.
                                                                                                                                                                                                                    PS00035; POU_1; PS00465; POU_2;
                                                                                                                                                                                                            PS50071;
                                                                                                                                                                                                                                       PS00027; HOMEOBOX_1;
                                      410
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43
54
71
111
111
127
127
172
254
 Conservative
                                      AA;
                                                                                                                                                                                                  homeobox;
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                                                                                                                                                                        DNA-BINDING;
                                                                                                                                                                                                   HOMEOBOX_
meobox; 1.
                                                                                                                                                                                                                            POU_1;
         3.3%;
                                                51
89
80
120
130
130
1405
1665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ion of four members of the POU family of and phorbol 12-myristate 13-acetate-tre
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                                     MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y., EDDY I
Score 118; DB 1;
Pred. No. 3.36e-01;
23; Mismatches 35
                                                                                                                                                                                                                                                                                                                is not removed
                                              HOMEOBOX.
C -> S (1
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POLY-SER.
POLY-GLY.
POLY-GLY.
POLY-GLY.
POU-IV BOX.
POLY-HIS.
POLY-SER.
                                                                            POU
                                                                                    POLY-HIS.
                                                                                                                                                                        HOMEOBOX
                                      48FFA52D
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ressed in a
                                                                           DOMAIN.
                                               G (IN REF.
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                                      CRC32;
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                                           2).
2).
                                                                                                                                                                                                                                                                                                               Usage
                  Length 410;
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Indels
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MBL outstation -
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Gaps
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                                                                                   RESULT
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Best Local :
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  SPOT_MYCPN
P75386;
01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00027; HOMEOBO
PROSITE; PS50071; HOMEOBO
PROSITE; PS00035; POU_1;
PROSITE; PS00465; POU_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTER
TELEDOSTEI; GUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; CYPRINOIDEA;
CYPRINIDAE; RASBORINAE; DANIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U43898; G1399384; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAMPATH K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 96193692.
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                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMEOBOX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- TISSUE SPECIFICITY: NERVOUS SYSTEM
-!- DEVELOPMENTAL STAGE: EXPRESSED EAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BIOCHEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Developmental expression of class III and
                                                                                                                                                                                                                   201 MDHHHHHHHHQHHAG-VNSHDSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHEM. BIOPHYS. RES. COMMUN. 219:565-571(1996) FUNCTION: MAY PLAY A ROLE IN SPECIFYING TERM!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEURONAL PHENOTYPES (BY SIMILARITY). SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: STRONG TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TO CLASS-3 POU.
                                                                                                                                                                 MGHHHHHHHHHSSGHIDDDDKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RITLTYKEGAPITIMD-NGNIDTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00046; homeobox; PF000157; pou; 1. P14859; 1POU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HHHHHHHHHSSGHIDDDDKHMKKISSVIAI-ALFGTIATANAADLTASTTATATLVEPA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U43656; G1323758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                    406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STUART G.W.;
  (REL.
                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOMEOBOX_1;
HOMEOBOX_2;
POU_1; 1.
POU_2; 1.
pmeobox; 1.
  35, CREATED)
                                                                                                                                                                                                                                                                                              3.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tatement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                  43677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSCRIPTION REGULATION; NUCLEAR PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                  MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER "POU" TRANSCRIPTION
                                                                                                                                                                                                                                                               Score 114; DB 1; L
Pred. No. 9.11e-01;
4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                        POLY-ALA.
POLY-HIS.
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                                                       733 AA
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Query Match
Best Local
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01-OCT-1993
01-OCT-1996
15-JUL-1998
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**PUNCTION: IN EUBACTERIA PPGPP (GUANOSINE 3'-DIPHOSPHATE 5-'DIPHOSPHATE) IS A MEDIATOR OF THE STRINGENT RESPONSE THAT COORDINATES A VARIETY OF CELLULAR ACTIVITIES IN RESPONSE TO CHANGES IN NUTRITIONAL ABUNDANCE. THIS ENZYME CATALYSES THE DEGRADATION OF PPGPP INTO GDP: IT MAY ALSO BE CAPABLE OF CATALYZING THE SYNTHESIS PPGPP (BY SIMILARITY).

-!- COPACTOR: MANGANESE (BY SIMILARITY).
                                                                                                                              01-OCT-1993 (REL. 27, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE
NUCLEAR TRANSPORT PROTEIN NIP1.
NIP1 OR YMR309C OR YM9924.01C OR YM9952.11C.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
SEQUENCE FROM N.A. MEDLINE; 93066237.
                                                                                                           EUKARYOTA;
                                                                                                                                                                                                                                                                                                                       NIP1_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYDROLASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete sequence analysis of the genome of the bacterium {\tt Mycoplasma} pneumoniae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIMMELREICH R., HILBERT H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE; 97105885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYCOPLASMA PNEUMONIAE. BACTERIA; FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01.NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01.NOV-1997 (REL. 35, LAST ANDOTATION UPDATE)
01.NOV-1997 (REL. 35, "ENIS (DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE
02.1.7.2) ((PPGPP)ASE) (PENTA-PHOSPHATE GUANOSINE-3'-
                                                                                  SACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000043; G1674128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBI outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way iffed and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --QLTGHGSSVLEELV-QLVKDKNIDISIKYDPRKDSEVFANRVITDDIELLKKILAYF-
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                                                                                                        FUNGI; ASCOMYCOTA; HEMIASCOMYCETES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               733 AA;
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larity 27.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 113; DB 1;
Pred. No. 1.16e+00,
34; Mismatches 4:
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                                                                                                        SACCHAROMYCETALES
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Q99074;

Q1-JUN-1994 (REL.

Q1-JUN-1994 (REL.

Q1-JUN-1994 (REL.)
                      SEQUENCE FROM N.A.
STRAIN-REGEL; TISSUE-SPORE;
MEDLINE; 92033077.
MEDLINE; 92033077.
MEDLINE; 92033077.
MIGHELMORE R.W.;
"Highly abundant and stage-specific mRNAs in Bremia lactucae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
CONFLICT
CONFLICT
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CHURCHER C.M., LOUIS E.J., BARRELL B.G., RAJANDREAM M.A.,
SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH SUBMITTED (APR-1995) TO EMBL/GENBARK/DOBJ DATA BANKS.
-!- FUNCTION: INVOLVED IN TRANSPORT OF PROTEINS TO THE NUCLEUS;
PROBABLY VIA ITS SERINE-RICH ACIDIC N-TERMINAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GU Z., MOERSCHELL R.P., SHERMAN F., GOLDFARB D.S.; "NIP1, a gene required for nuclear transport in yeast."; PROC. NATL. ACAD. SCI. U.S.A. 89:10355-10359(1992).
                                                                                                                                                                                                  BREMIA.
                                                                                                                                                                                                                      BREMIA LACTUCAE (LETTUCE EUKARYOTA; STRAMENOPILES;
                                                                                                                                                                                                                                                                          HAM34.
                                                                                                                                                                                                                                                                                              HAM34
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EMBL; Z54141; G984682; -.
EMBL; Z49212; G798851; -.
PIR; A46417; A46417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=S288C / AB972;
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SUBCELLULAR LOCATION: CYTOPLASMIC; N
SIMILARITY: TO S.POMBE SPACIEI1.01C.
  PLANT MICROBE INTERACT. 3:225-232(1990).
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31; Conse
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29, LAST SEQUENCE UPDATE)
29, LAST ANNOTATION UPDATE)
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; OOMYCETES; PERONOSPORALES; PERONOSPORACEAE;
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V -> D (IN I
Q -> H (IN I
K -> N (IN I
K -> N (IN I
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                                                                                                                                                                                                                  EMBL; X16984; G2488; -. SPORULATION; STRUCTURAL
                                                                                                                                                                                                    SEQUENCE
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85
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                                                                                               1 MKFSQILVLAAIAVAAISAQDAAPATTPDTATATTPAAATTTTTTTTPAADAGTASTEQT 60
                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: COULD BE A STRUCTURAL PROTEIN REQUIRED FOR THE INFECTION PROCESS OF B.LACTUCAE.
TISSUE SPECIFICITY: GERMINATING SPORES.
LLVGTLTLGGYKTGTTSTSVNFTDAAGDPMYLTFTSQDGNNHQFTTKVIGKDSRD 139
                               TTAGPEAAGATNGTTTTPPADGTQTATAPLDATATEESSASGEMTPTV-GTDTSD 114
                                                                  KKISSVIAIALFGTIATANAADLTASTTATATLVEPARITLTYKEGAPITIMDNGNIDTE
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28; Conser
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173 AA; 1647
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28; 1
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Search completed: Sat Nov 27 15:35:00 1999 Job time: 43 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Nov 27 15:35:18 1999; MasPar time 32.46 Seconds 876.148 Million cell updates/sec

Tabular output not generated.

Sequence: Description: Perfect Score:

Scoring table: PAM 150 Gap 11

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembl9
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 51.021; Variance 127.664; scale 0.400

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 2 3 3 4 4 4 4 6 6 6 7 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
22547 22132 22132 22125 22124 2074 653 168 1133 1133 1133 1128 1128 1129 1129 1129 1129 1129	Score
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324 325 325 324 324 324 324 324 324 324 324 324 324	Length
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CODED FOR BY C. ELEGAN TRANSCRIPTION FACTOR.		HYPOTHETICAL PROTEIN M	INVASIN.	PUTATIVE G-PROTEIN.	FISSION YEAST.	HYPOTHETICAL 47.2 KD P	HYPOTHETICAL 31.2 KD P	ROMPA (FRAGMENT).	DHC7.	AARP1 PROTEIN (FRAGMEN	KIAA0570 PROTEIN.	TF125 PROTEIN.	PUTATIVE G-PROTEIN.	RIBOSOMAL PROTEIN SO1.	HYPOTHETICAL 47.2 KD P	POT. ORF I.	ROMPA (FRAGMENT).	SIROHEME SYNTHASE.	PUTATVE SENSORY TRANSD	MYOSIN HEAVY CHAIN.	LMP3 PROTEIN.	CYTOTOXIN ASSOCIATED P	DNA-DIRECTED RNA POLYM
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ALIGNMENTS

Dβ	ργ	Oy Db	g b	Db	Ma Be	SQ	DR	RA RL	RA C	R P	RN	88	င္ပ	SO	GN E	ij	DT.	DT	A L	RESULT
241 GSENKRTGALGNLKNSYSYNKDNNELSHFATTCSDKSRPLNDLVSQKTTQLSDITSRENS 300	181 SGTINIHDKSINLMDKNLYGYTDEEIFKASAEYKILEKMPQTTIQVDGSEKKIVSIKDFL 240	121 VMHFSLTADRIDDDILKVIVDSMNHHGDARSKLREELAELTAELKIYSVIQAEINKHLSS 180 	61 NRVITDDIELLKKILAYFLPEDAILKGGHYDNQLQNGIKRVKEFLESSPNTQWELRAFWA 120 	1 MIRAYEQNPOHFIEDLEKVRVEQLTGHGSSVLEELVQLVKDKNIDISIKYDPRKDSEVFA 60 	Query Match 63.4%; Score 2247; DB 2; Length 326; Best Local Similarity 99.7%; Pred. No. 0.00e+00; Matches 325; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE 326 AA; 37240 MW; 443BDEDC CRC32;	053946; G2996251;	KOBAYASHI A., CARRANO A.V., BRUBAKER R., GARCIA E.; SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.	HU P., ELLIOTT J., MCCREADY P., SKOWRONSKI E., GARNES J.,	SEQUENCE FROM N.A.	[1]	BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE; YERSINIA.	PLASMID PCD1.	YERSINIA PESTIS.	LCRV.	(TREMBLREL.	(TREMBLREL. 07,	1998 (TREMBLREL.	O68697:	

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Q1-NOV-1996 (TREMBLREL.
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INFECT. IMMUN. 65:446-451(1997).
EMBL; X96801; E239988; -.
SECUENCE 324 AA; 37162 MW; 5
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INFECT. IMMUN. 65:446-4
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ROGGENKAMP A., GEIGER A.M., LEITRITZ L., KESSLER A., HEESEMANN Passive immunity to infection with Yersinia spp. mediated by anti-recombinant V antigen is dependent on polymorphism of V
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ROGGENKAMP A., GEIGER A.M., LEITRITZ L., KESSLER A., HEESEN "Passive immunity to infection with Yersinia spp. mediated anti-recombinant V antigen is dependent on polymorphism of
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larity 92.8%;
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J. BACTERIOL. 179:7165-7168(1997).
EMBL; AF010149; G2459968; ...
SEQUENCE 294 AA; 32283 MW; 0FAD2082 C1
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Q16256
Q16256;
01-NOV-1996
01-NOV-1996
01-NOV-1998
01-NOV-1998
WT1-WILMS' TU
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MEDLINE; 95166649.
HAMILTON T.B., BARILLA I
"High affinity binding of the second 
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030527;
01-JAN-1998
01-JAN-1998
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MEDLINE; 98037517
YAHR T.L., MENDE-
                                                                                                           NUCLEIC ACIDS RES. 23:277-284(1995)
EMBL; S75264; G896247; -.
PROSITE; PS00028; ZIT-GINGER_C2H2;
PFAM; PF00096; ZIT-C2H2; 4.
ZINC-FINGER; METAL-BINDING; DNA-BINI SEQUENCE 168 AA; 20165 MW; E860;
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PCRV.
PSEUDOMONAS AERUGINOSA.
BACTERIA; PROTEOBACTERIA;
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CATARRHINI;
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     Conservative
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                            4.78;
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No. 1
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No. 1.64e-79;
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SEQUENCE FROM N.A.
LIN J.W., WYSZYNSKI M., MADHAVAN R., SEALC
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ
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SEQUENCE 1642 AA; 191023 MW; 99E0E48C
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EUKARYOTA; METAZOA; CHORDATA;
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SEQUENCE FROM N.A.
WU X., GRAVES T., BRADSHAW H.;
"The sequence of Homo sapiens BAC clone RG293F11.";
"The sequence of Homo sapiens BAC clone RG293F11.";
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EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TREMBLREL 07, CREATED)
01-AUG-1998 (TREMBLREL 07, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)
KIAA0594 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                060335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              code for large proteins in vitro.";
DNA RES. 5:31-39(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATARRHINI; HOMINIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAGASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OHARA O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                       431 EQRRHLEEQLKEIHRKLQAVDSGLIALRETSKHLEHKDN-ELRQKKKELLERKTKK-RQL 488
                                                                                                                                                                   458
                                                                                                                                                                                                                  548
                                                                                                                                                                                                                                                                 400
                                                                                                                                                                                                                                                                                                                489
                                                                                                                                                                                                                                                                                                                                                               343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVDLILQNTTVISEKNKLESDYMAA-SSQLRLTEQHFIELDENRQRLLQKCKELMKR
                                                                                                                                                                                                                                                                                                                                                  DARSKLREELAELTAELK-IYS-VIQA-EINKHLSSSGTINIHDKSINLMDKNLYGYTDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LNIKLQDTNSQKEKLKEELG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPNT-QW--ELRAFMAVMHFSL-TADRIDDDILKVIVDSMNHHGDAR-SKLREELAELTA
                                                                                                                                                                {\tt NNELS-HFATTCSDKSRPLNDLVSQKTTQLSDITSRFNSAIEALNRFIQKYDSVMQR}
                                                                                                                                                                                                                                                                                         EQ-KISSKLGSLKLMEQDTCNLEEEERKASTKIKEINVQKAKLVTELTNLIKICTSLHIQ 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTIQVDGSEKKIVSIKDFLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RKDSEVFANRVITDDIELLKKILAYF - - LPEDTILKGGHYDNQLQ - N - GIKRVK - EFLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IQEKETIIIEELNTKIIEEEKKTLELKDKLTTADKLLGELQEQIVQKNQEIKNMKLELTNS : | : : | | | | : | : : |
                                                                                                                                                                                                                                                              EIFKASAEYKILEKMPQTTIQVDGSEKKIVS-IKDFLGSENKRTGALGNL-KNSYSYNKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELKIYSVIQAEINKHLSSSGTINIHDKSINLMDKNLYGYTDEEIFKASAEYKILE-KMPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KQKERQSSEEIKQLMGTVE-ELQKRNHKDSQFETDIVQRMEQETQRKLEQLRAELDEMYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AB011166; D1026450; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T., ISHIKAWA K., MIYAJIMA N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 3.8%;
Similarity 21.9%;
57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98290545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      882 AA;
(TREMBLREL.
                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104906 MW;
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Pred.
79; M
CREATED)
LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 128; DB 4;
Pred. No. 6.05e-02;
                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84CC9E80 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e 133; DB 4; Length 16.
. No. 1.69e-02; .
Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                     1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TANAKA A.,
                                                                     ΑA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KOTANI H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOMURA N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT
AC 088
AC 080
DT 01
DT 01
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CE EL
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COC CE
RR CC CC

Search completed: Sat Nov Job time: 101 secs.
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Best Local S
Matches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.6%;
Best Local Similarity 47.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
WOLLA J., XU Q., HARTER K., GRUISSEM W., LUAN S.;
"Genes for calcineurin B-like proteins in Arrabidopsis are differentially regulated by stress signals.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF076253; G3309086;
SEQUENCE 226 AA; 26031 MW; F51F2707 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILT 15

081447;

081447;

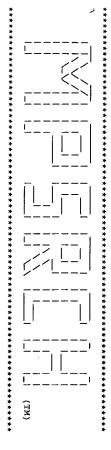
01-NOV-1998

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01-NOV-1998

CALCINEURIN E

CBL3:
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ORF YOL087C FROM CHROMOSOME XV.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANTAE; STREADPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBMITTED (JUL-1996) TO ENEMBL; X83121; G600471; -. EMBL; Z74829; E251885; -. SEQUENCE 1116 AA; 12538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
ZUMSTEIN E., PEARSON
SUBMITTED (JUL-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZUMSTEIN E., PEARSON B.M., KALOGEROPOULOS A., "A 29.425 kb segment on the left arm of yeast more than twice as many unknown as known open yeasT 11:975-986(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-FY1679;
MEDLINE; 96021609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                      251
                                                                                                                                                                                      185
                                                                                                                                                                                                                                       194
                                                                                                                                                                                                                                                                                          125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                365 HHHHHHHEHEEQNISTTDAKVKKYGGILDIALL 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 HHHHHHHHHSSGHIDDDDKHMKKISSVIAIALF 36
                                                                                                                                                                                                                                 SEVFANRVITDDIELLKKI-LAYFLPEDTILKGGHYDNQLQN 291
                                                                                                                                                                                 KEEWRTLVLRHP-SLLKNMTLQYLKDITTTFPSFVFHSQVED 225
                                                                                                                                                                                                                                                                                                                                       h 3.5%;
Similarity 26.5%;
27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TREMBLREL 08, CREATED)
(TREMBLREL 08, LAST SEQUENCE UPDATE)
(TREMBLREL 08, LAST ANNOTATION UPDATE)
B-LIKE PROTEIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TO EMI
                                                     27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125381 MW;
                                                     15:36:59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M., KALOGEROPOULOS EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                       Score 123; DB 10;
Pred. No. 2.11e-01;
28; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 127; DB 3;
Pred. No. 7.78e-02;
7; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         099CF031 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA
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                                                                                                                                                                                                                                                                                                                                          42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCHWEIZER
'A BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCHWEIZER M.; chromosome XV contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reading frames.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1116;
                                                                                                                                                                                                                                                                                                                                                                                        Length 226;
                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                       5
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```



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Sat Nov 27 15:30:18 1999; MasPar time 20.48 Seconds 541.086 Million cell updates/sec

Description: Perfect Score: >US-08-699-716A-2 (1-521) from US08699716A.pep 3546 1 MGHHHHHHHHHSSGHIDDD......RFIQKYDSVMQRLLDDTSGK 521

PAM 150 Gap 11 170751 seqs, 21266608 residues

Scoring table: Sequence:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 35.735; Variance 201.794; scale 0.177

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			מל
12 14 15	10 9 8	7 O U 4 U D V	Result No.
971 968 968 966 867	1100 1100 1100 971	3166 2242 2242 2236 2233	Score 3294
27.4 27.3 27.3 27.2 24.5			. o
150 151 151 151 192	170 170 170 149	480 329 329 329	Length 501
14 14 34	3344	19 15 15 16	DB 19
W59787 W01042 R76526 R76527 W59785	W59783 W59783 W59782	W01045 W01040 R79961 W01041 R79962	ID W01044
Amino acid sequence o Y. pestis Fl antigen. Yersinia pestis cafl Yersinia pestis cafl Amino acid sequence o	Yersinia pestis cafi Amino acid sequence o Amino acid sequence o Nucleotide sequence o		Description Y. pestis F1/V antiqe
1.42e-60 2.38e-60 2.38e-60 3.36e-60 7.78e-53	3.31e-70 3.31e-70 3.31e-70 3.31e-70 1.42e-60	1.17e-226 2.16e-156 2.16e-156 6.15e-156 1.04e-155	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
106	106	106	107	108	106	110	116	120	123	135	135	135	146	146	147	146	146	146	150	150	154	152	157	172	172	189	190	738
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mitosin	enhanced anti	AmI105 encoded by Ida	Streptococcus uberis	leobind	Borrelia burgdorferi	prot	ence of	Helicobacter polypept	10	Recombinant squirrel	squirr	squir		potu	nydomonas rei	FP505 protein contain	HFKT peptide.		botuli	A neuro	botul	botul	botul	Clostridium botulinum		a o	ne-entero	Amino acid sequence o
.71e+	. 7.1	.71e	.1	3.63e+01	. 7	. 7	2	36	. 90e	.37e	.37e	. 37e	. 99е	. 99е	.73e	. 99e	.99e	.99e	.12e	. 12	.34e	.45e	. 11e	.61e	.61e-	. 69	7e-	2.77e-43

ALIGNMENTS

88	88	3 3	r v	PT	DR	DR	PA A	PR	PR	PR	PF	PD	PN	FT	FΤ	FT	FT	ΕŢ	FT	FΤ	FT	FΤ	ΕT	ŦΤ	FT	FΗ	SO	SO	ΚW	X	DE	3 2	ää	RESULT
ion (T38249) usion protei	Yersinia pest tain its confo	Ę	- useful in vaccine for protection	pestis V antigen and F1 antige	N-PSDB; T38249.	WPI; 96-433824/43.	UK SEC FOR DEFENCE.	1995; GB-024		MAR-1995;	MAR-1996;	19-SEP-1996.		/note= "m							/label= Fl_antigen		/note= "F1 a	/label= Sig_peptide	tide		synthetic.	Chimeric Yersinia pestis strain GB;	gen; caf1.	igue; vacci	Y. pestis F1/V antigen fusion.	28-DEC-1996 (first entry)	W01044 standard; Protein; 501 AA.	•

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Matches
19-SEP-1996: G00571.
13-MAR-1996; GB-005059.
13-MAR-1995; GB-018946.
05-DEC-1995; GB-018946.
05-DEC-1995; GB-024825.
(MINA) UK SEC FOR DEFENCE.
Beckett AM, Leary SEC, Oyst
                                                                                                                                                            28-DEC-1996
Y. pestis F1
Plague; vacc
Fl antigen;
Chimeric Yer
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Sequence
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W01045 standard;
W01045;
                                                                                                                                     protein
                                                                                                                                              Key
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larity 98.4%;
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  Oyston
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2; M
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  PCF,
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1. No. 2.07e-
Mismatches
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                                                                                                                   antigen"
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NR N-PSDB; 738256.

RN-PSDB; 738256.

PT Versinia pestis V antigen and Fl antigen or their protection against plague perticipate parts - useful in vaccine for protection against plague PS Disclosure; Page 51-55; 98pp; English.

CC A fusion protein (W01045) comprises the Fl antigen (see also W01042) and V antigen (see also W01041) of Yersinia pestis joined CC by a linker that allows each protein to attain its conformational CC state. It is the product of a gene fusion (T38256) obtd. by PCR CC amplification of Y. pestis DNA. FI/V fusion protein can be CC expressed by gut-colonising organism transformants, to induce
RESULT RESULT AND ACCOUNTS OF STATE AND ACCO
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Matches
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W01040 standard; Prot
W01040;
28-DEC-1996 (first e
Y. postis V antigen.
Plague; vaccine; gene
Fl antigen.
                                                                              WO9628551-A1.
19-SEP-1996.
13-MAR-1995;
13-MAR-1995;
15-SEP-1995;
05-DEC-1995;
(MINA) UK SEC FOR DEFENCE. Bennett AM, Leary SEC, Oy WPI; 96-433824/43. N-PSDB; T38242.
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95; GB-005059.
95; GB-018946.
95; GB-024825.
K SEC FOR DEFEN
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llarity 98.3%;
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Recombinant DNA expressing Yersinia pestis V antigen - useful in oral or parenteral vaccines for protection against plague Claim 6; Page 11-13; 25pp; English.
R79961-62 are encoded by T04222-23 (resp.), DNA sequences (lcrV) encoding all or a protective epitopic part of the mature V protein of Yersinia pestis. The protein was expressed as a fusion protein with maltose binding protein or glutathioner-S-transferase in 3 different plasmid vectors. Y. pestis is the highly virulent causative organism of plague in a wide range of animals, including man. The V antigen (LcrV) is an unstable 37.3 kDa monomeric peptide encoded on the ca. 70 kb Lcr plasmid. The V antigen is postulated to act as a virulence antigen, and transformed microorganisms contg. recombinant DNA encoding a V antigen protein/peptide are useful in vaccines to protect against plague.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Partial LcrV (V a LcrV; V antigen; Yersinia pestis.
                                                                                                                                                                                                                                                                                                                                                                                                     (MINA ) UK SEC FOR DEFENCE.
Leary SEC, Titball RW, Williamson
WPI: 95-328268/42.
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14-SEP-1995.
06-MAR-1995; G00481.
08-MAR-1994; GB-004577
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Partial LcrV (V antigen) of
LcrV; V antigen; virulence;
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Recombinant DNA expressing
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Yersinia pestis V antigen (W01040) is capable of evoking prof
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19-SEP-1996;
13-MAR-1996; G00571.
13-MAR-1995; GB-005059.
15-SEP-1995; GB-018946.
05-DEC-1995; GB-024825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W01041 standard; W01041;
                                                                                                                        resinia pestis V antigen and Fl antigen or their protective epitopic parts - useful in vaccine for protection against plague Disclosure; Page 32-35; 98pp; English.

Yersinia pestis V antigen (W01041) is capable of evoking protective immune responses in animals. A combined vaccine of V and Fl antigens (see also W01042) can at least match the protection afforded by live attenuated EV76 vaccine without any of the hazards that have kept the EV vaccine from general use. The V antigen is produced using the lcrV gene (see also T38243) obtd. from Y. pestis by PCR amplification. It can also be prepd. as a fusion with Fl antigen (see also W01044-45) and expressed by attenuated AroA or C salmonella tymphi and gut-colonising bacteria for protection against
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WPI; 96-433824/43.
N-PSDB; Т38243.
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Y. pestis V
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R. No. 6.15e-156;
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                                                                                                                                                                                                                                                                PT Recombinant DNA expressing Yersinia pestis V antigen - useful in PT oral or parenteral vaccines for protection against plague
PS Claim 6; Page 15-16; 25pp; English.
CC R79961-62 are encoded by T0422-23 (resp.), DNA sequences (lcrV) encoding CC all or a protective epitopic part of the mature V protein of Yersinia CC pestis. The protein was expressed as a fusion protein with maltose CC binding protein or glutathione-S-transferase in 3 different plasmid CC vectors. Y. pestis is the highly virulent causative organism of plague in a wide range of animals, including man. The V antigen (LcrV) is an CC unstable 37.3 kDa monomeric peptide encoded on the ca. 70 kb Lcr plasmid. The V antigen is postulated to act as a virulence antigen, and CC transformed microorganisms contg. recombinant DNA encoding a V antigen protein/peptide are useful in vaccines to protect against plague.
SC Sequence 329 AA;
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Best Local S
Matches 32
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14-SEP-1995; 06-M^~
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08-MAR-1994; GB-004577.

(MINA ) UK SEC FOR DEFENCE

Leary SEC, Titball RW, W

WPI; 95-328268/42.
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No. 1
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19-SEP-1996; G00571.

13-MAR-1996; GB-005059.

15-SEP-1995; GB-018946.

05-DEC-1995; GB-024825.

(MINA) UK SEC FOR DEFENCE.

Bennett AM, Leary SEC, Oys.
WPI; 96-433824/43.

N-SDB; T38248.
23-DEC-1994; G02818.
24-DEC-1993; GB-026425.
(MINA) UK SEC FOR DEFENCE.
Howells A, Leary SEC, Oyst
WPI; 95-246396/32.
                           17-DEC-1995 (first en
Yersinia pestis caf1 (
Vaccine; antigen; Salm
bubonic plague; pneumo
Yersinia pestis.
W09518231-A1.
06-JUL-1995.
23-DEC-1994; G02818.
24-DEC-1993; GB-026425
                                                                                                                                                                                                                                                                                                                            Yersinia pestis V antigen and F1 antigen or their protective epitopic parts - useful in vaccine for protection against plague Example 2; Page 61-62; 98pp; English.

The F1 antigen (W01043), including the signal peptide, of Yersini pestis was produced from a DNA sequence (T38248) obtd. by PCR amplification (see also T38257-58) of Y. pestis DNA. Expression of the F1 antigen (see also W01042) by gut-colonising organisms including humans, against plague.
                                                                                                                   R76528
                                                                                                                             R76528
                                                                                                                                                                                                                                                                                                                       Sequence
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Y pestis Fl
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vaccine;
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nes 170; Conservative
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                                                                            Salmonella typhimurium; neumonic plague.
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. No. 3.31e-70;
Mismatches 0;
            Titball
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F1 antigen;
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Disclosure; Page 20; 27pp; English.

The sequence represents the Y. pestis caf1 (F1) antigen expressed from plasmid pFORF1b. The DNA construct can be used to transform human or animal gut colonizing microorganisms, specifically attenuated Salmonella typhimurium or Salmonella typhi. The transformed microorganisms can be used as live/attenuated vaccines which induce immune responses at mucosal surfaces. The vaccines provide protection against infection with Y. pestis, and are parenterally and orally active vaccines offering protection
                                                                                                                                                                                                                                                                                                                                                         Protection of animals against plague - using nucleic acid encoding antigen from Yersinia, Pasteurella and Francisella spp.
Disclosure; Pages 53-54; 75pp; English.
This is the amino acid sequence of a Yersinia pestis F1 antigen, used in the method of the invention. Plasmid and host cells are used to produce recombinant antigens, especially Yersinia pestis antigens. The recombinant antigens can be used in vaccines that are capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-OCT-1998 (first entry)
Amino acid sequence of Fl antigen nYpFlsec510.
Fl antigen; plasmid; vaccine; plague; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HESK-) HESKA CORP.
Haanes EJ, Osorio JE,
WPI; 98-333331/29.
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04-DEC-1996; US-767115.
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Sequence
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DNA constructs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q92819
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                                                                                                                                                                                                                                                                                                            an animal from
170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 AA;
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                                                                                                                                                                                                 Score 1100; DB 34;
Pred. No. 3.31e-70;
0; Mismatches 0;
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No. 3.31e-70;
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                                                                                                                       N-PSDB; V41609.

N-PSDB; V41609.

Protection of animals against plague antigen from Yersinia, Pasteurella and antigen from Yersinia, Pasteurella and antigen from Yersinia, Pagana 63; 75pp; English.
                                                                                                                                                                                                                                                                                                       11-JUN-1998.
04-DEC-1997;
04-DEC-1996;
                                antigen from Yersinia, Pasteurella and Francisella spp. Claim 10; Page 63; 75pp; English.

This is the amino acid sequence of a Yersinia pestis Fl antigen, using the method of the invention. Plasmid and host cells are used the produce recombinant antigens, especially Yersinia pestis antigens. The recombinant antigens can be used in vaccines that are capable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protection of animals against plague - using nucleic acid encoding antigen from Yersinia, Pasteurella and Francisella spp. Claim 10: Page 52: 75pp English.

This is the amino acid sequence of a Yersinia pestis F1 antigen, using the method of the invention. Plasmid and host cells are used the produce recombinant antigens, especially Yersinia pestis antigens. The recombinant antigens can be used in vaccines that are capable protecting an animal from contracting plague.
                                                                                                                                                                                                                       (HESK-) HESKA CORP.
Haanes EJ, Osorio JE,
WPI; 98-333331/29.
                                                                                                                                                                                                                                                                                                                                                                               F1 antigen; plasmid; Yersinia pestis. WO9824912-A2.
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11-JUN-1998.
04-DEC-1997; U22617.
04-DEC-1996; US-767115.
            protecting an animal from contracting plague
                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of F1 antigen; plasmid; va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W59788;
26-OCT-1998
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Sequence
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N-PSDB; V41594.
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l Similarity 100.0%;
170; Conservative
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of F1 antigen pypF1sec170.
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No. 3.31e-70;
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Francisella sp
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13-MAR-1995;
13-MAR-1995;
15-SEP-1995;
05~DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protection of animals against plague - using nucleic acid encoding antigen from Yersinia, Pasteurella and Francisella spp. Claim 10; Page 60; 75pp; English.

This is the amino acid sequence of a Yersinia pestis Fl antigen, usin the method of the invention. Plasmid and host cells are used to produce recombinant antigens, especially Yersinia pestis antigens.
                                                                                                                                                                                                                                                                                                                                                                            W01042;
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Sequence 150 AA;
                                                                                                                                                                    WO9628551-A1.
                                                                                                                                                                                                       Yersinia
                                                                                                                                                                                                                                                                          Plague;
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04-DEC-1996; US-767115.
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Amino acid sequence of F1 antigen pypF1mat150
F1 antigen; plasmid; vaccine; plague.
                                                                                                                                     19-SEP-1996.
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Local Similarity 100.0%;
hes 149; Conservative
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Pred. No. 1.42e-60;
0; Mismatches 0
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Pred. No. 1.42e-60;
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Y Persinia pestis V antigen and Fl antigen or their protective
Y Disclosure; Page 43 45; 98pp; English.
Y Persinia pestis Fl antigen (W01042) is capable of evoking protective
Y Cersinia pestis Fl antigen (W01042) is capable of evoking protective
I antigens (see also W01040-41) can at least match the protection
I cafforded by live attenuated EV76 vaccine without any of the hazards
I that have kept the EV vaccine from general use. The Fl antigen is
I produced using the cafl gene (see also T98244) obtd. from Y.
I can also be prepd. as a fusion with
I v antigen (see also W01044-45) and expressed by attenuated AroA or
I cagainst plague. Expression by gut-colonising bacterial transformants
I can readence a readency v persits.
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Bennett AM,
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N-PSDB
                                                                                                                                                                                                                                                                                                                                          The sequence represents the Y. pestis cafl (F1) antigen expressed from plasmid proxized. The DNA construct can be used to transform human or animal gut colonizing microorganisms, specifically attenuated Salmonella typhimurium or Salmonella typhi. The transformed microorganisms can be used as live/attenuated vaccine; which induced impune responses at musced as live/attenuated vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bubonic plague; pneumonic plague
Yersinia pestis.
W09518231-A1.
                                                                                                                                                                                                 which induce immune responses at mucosal surfaces. The vacci
provide protection against infection with Y. pestis, and are
parenterally and orally active vaccines offering protection
against bubonic and pneumonic plague.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MINA ) UK SEC FOR DEFENCE.
Howells A, Leary SEC, Oys
WPI; 95-246396/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yersinia pestis cafl (F1) antigen.
Vaccine; antigen; Salmonella typhimurium;
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Sequence 151 AA;
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N-PSDB; T38244.
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Pred. No. 2.38e-60;
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No. 2.
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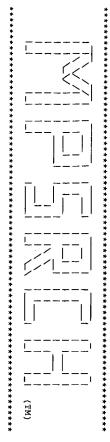
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Search completed: Sat Nov 27 15:32:40 1999 Job time: 142 secs.
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Best Local Similarity
Matches 148; Conser
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23-DEC-1994; G02818.
24-DEC-1993; GB-026425.
(MINA) UK SEC FOR DEFENCE.
Howells A, Leary SEC, Oystc
WPI; 95-246396/32.
N-PSDB; Q92818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA constructs capable of transforming microorganisms - which can be used as live or attenuated vaccines which induce an immune response, against Yersinia pestis, at mucosal surfaces.

Disclosure: Page 18: 27pp; English.

The sequence represents the Y. pestis cafl (F1) antigen expressed from plasmid pFSIG3a. The DNA construct can be used to transform human or animal gut colonizing microorganisms, specifically attenuated Salmonella typhimurium or Salmonella typhi. The transformed microorganisms can be used as live/attenuated vaccines which induce immune responses at tmucosal surfaces. The vaccines provide protection against infection with Y. pestis, and are parenterally and orally active vaccines offering protection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LT 15
R76527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               against bubonic and pneumonic plague.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bubonic plague; pneumonic plague.
Yersinia pestis.
W09518231-A1.
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17-DEC-1995 (first entry)
Yersinia pestis cafl (F1) antigen.
Vaccine; antigen; Salmonella typhimurium; Salmonella typhi;
                                                                                                                                                                                                                            103
                                                                                                                     164
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                                                                                                            standard; Protein; 151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.2%;
ilarity 98.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 966; DB 14; I
Pred. No. 3.36e-60;
2; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 151;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Nov 27 15:37:17 1999; MasPar time 8.24 Seconds 753.590 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-699-716A-2 (1-521) from US08699716A.pep 3546 1 мGHHHHHHHHHHSSGHIDDD.......RFIQKYDSVMQRLLDDTSGK 521

Scoring table: Sequence: PAM 150 Gap 11

Searched: 122461 seqs, 11912985 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Statistics: Mean 33.116; Variance 187.062; scale 0.177

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

22222222222222222222222222222222222222	1	Result
146 146 146 146 146 146 1146 106 106 106 106 107 108 98 98 98	150	Score
444466666666666666666666666666666666666	4.2	% Query Match 1
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sequence seq	Sequence	Description
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3.84e-6.87e-6.87e-6.87e-6.87e-6.87e-6.87e-6.87e-6.87e-6.87e-7.44-7.11.87e-7.44-7.11.87e-7.44-7.11.87e-7.44-7.11.87e-7.11	3.84e-02	Pred. No.

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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
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\vdash	Applicatio	Applicatio	Applicatio	Applicatio	Applicati	Applicati	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicati	Applicati	Applicatio						
6.99e+01	7.96e+01	7.96e+01	7.96e+01	6.14e+01	7.96e+01	٠		•	6.14e+01	٠	٠		6.99e+01	6.99e + 01	٠	6.99e+01		4.14e+01	4.14e+01	5.39e+01	5.39e+01

ALIGNMENTS

RESULT

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APPLICATION N FILING DATE: TTORNEY/AGENT NAME: INGOLI REGISTRATION	APPLICATION NUMBER: US 07/985,321 FILING DATE: 04-DEC-1992 PRIOR APPLICATION DATA:	APPLICATION NUMBER: US 08/161,907 FILING DATE: 02-DEC-1993 PRIOR APPLICATION DATA:	AFFLICATION NUMBER: US US/329,139 FILING DATE: 25-OCT-1994 PRIOR APPLICATION DATA:	CLASSIFICATION: 424 PRIOR APPLICATION DATA:	9 [TA:	SYSTEM: PC-DOS/MS-DOS	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	4104	STATE: CALIFORNIA	STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO	WEDLEN & CARROLL, LLP	CORRESPONDENCE ADDRESS:	OF INVENTION: NEUROTOXIN	TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM		Patent No. 5919665	Sequence 26, Application US/08405496A	sequence 20, Apprication US/08403496A			XXXXXX		US-08-405-496A-26 STANDARD: PRT: 462 AA.

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                COMPUTER: Floppy u.s.,
MEDIUM TYPE: Floppy u.s.,
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,604A
PTI.TING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26, Application US/08480604A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26, Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: OP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 795-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                    APPLICATION NUMBER: US 08/
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 16-MAR-1995
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                                                                                                                                                                                                                                                                                                 STREET: 220 MULTICOLOR CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: UNITED STATI ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 462 AA; 53932 MW; 1087243 CN;
                     FILING DATE: 02-DEC-PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                         APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
                                                                                                                                                                FILING DATE: 07-JUN-1995

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/422,711
                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acid
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                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: MEDLEN & CARROLL, LLP STREET: 220 MONTGOMERY STREET, SUITE
ING DATE: 04-DEC-1992 APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H: 462 amino acids amino acids LOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KINK, JOHN A
                                                                                                                                                                                                                                                                                                                        UNITED STATES
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                                               02-DEC-1993
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                        US 07/985,321
                                                                                                                                  US 08/405,496
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Pred. No. 3.84e-02;
7; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21, Application US/08651818A
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                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 594000.
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Local Similarity 59.4%;
nes 19; Conservative
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                                                            TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO:
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REFERENCE/DOCKET NUMBER: 0PHD-01763
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Carroll, Peter G.
                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                   APPLICANT: de Boer, Piet A.J.
APPLICANT: Hale, Cynthia A.
TITLE OF INVENTION: COMPOSITIONS AN
TITLE OF INVENTION: ANTIMICROBIALS
                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein 
TENCE 462 AA; 53932 MW; 1087243 CN;
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ATTORNEY/AGENT INFORMATION:
                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                      CITY:
STATE:
                                                                                                                                                  FILING DATE: CLASSIFICATION: 530
                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                 COUNTRY: UZIP: 94104
                TYPE: amino acid
STRANDEDNESS: not
                                                                                                       REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: CASE-02249
                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE:
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                                       LENGTH:
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                                                                                                                                                                                                                                                                                          220 Montgomery Street, Suite 2200
                                     21 amino acids
                                                                                                                                                                                                                                                            United States of America
         not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                             Floppy disk
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31-OCT-1989
                   not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 150; DB 1; Lenv. Pred. No. 3.84e-02;
                                                                                                                                                                        US/08/651,818A
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                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24, Application US/08405496A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                             TOPOLOGY: li
MOLECULE TYPE:
QUENCE 23 AA; 2
                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 02-DEC-1993
                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 16-MAR-19
                                                                                                                                                                          APPLICATION NUMBER: US 07/429,791 FILING DATE: 31-OCT-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: WILLIAMS, JAMES A. TITLE OF INVENTION: VACCINE F TITLE OF INVENTION: NEUROTOXI
                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 04-DEC--
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                   REFERENCE/DOCKET NUMBER: OPHD-01308 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGHHHHHHHHHHSSGHID 18
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 0: FILING DATE: 25-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                            TYPE: amino a STRANDEDNESS:
                                                                                                                                                        NAME: INGOLIA, DIANE REGISTRATION NUMBER:
                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                 94104
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5919665
                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                             (415) 705-8410
(415) 397-937
                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 MONTGOMERY STREET,
                                                                                23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLEN & CARROLL,
                                                    linear
                               : protein
2741 MW; 2386 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.18;
94.48;
 4.18;
79.28;
                                                                                                                                                                                                                   NUMBER: US 07/985,321
04-DEC-1992
                                                                                                                                                                                                                                                                                                                             16-MAR-1995
                                                              unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEUROTOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VACCINE FOR CLOSTRIDIUM BOTULINUM
                                                                                                                                                                                                                                                                                             US 08/329,154
                                                                                                                                                                                                                                                                                                                                                           Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30
                                                                                                                                                                                                                                                              US 08/161,907
                                                                                                                                                                                                                                                                                                                                     US/08/405,496A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 144; DB 2; Le
Pred. No. 9.19e-02;
M:smatches 0;
Score 146; DB 2;
Pred. No. 6.87e-02;
                                                                                                                                                      40,027
                                                                                                       24:
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RESULT
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                                                                                                                               TELEFAX: (415) 397-83
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/
FILING DATE: 16-MAR-1995
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APPLICANT:
APPLICANT:
                                                                                                                                                                                            TELEPHONE: (415) 705-8410
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PRIOR APPLICATION DATA:
APPLICATION UNMEER: US 07/429,791
FILING DATE: 31-OCT-1989
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CURRENT APPLICATION DATA:
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                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 02-DEC-1993 PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 25-OCT
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
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TYPE: amino acid
STRANDEDNESS: un
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O MONTGOMERY STREET, SUITE
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25-OCT-1994
                                                                                                                                                                 397-8338
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Best Local S
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  US-08-651-818A-23
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MOLECULE TYPE:
SEQUENCE 23 AA;
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                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19, Application US/08651818A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19
Patent No.
GENERAL II
                                                                                          Match 4.1%;
Local Similarity 79.2%;
                                                                                                                                                                                               TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 53 amino acids
TYPE: amino acid
                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: CASE-02249
TELECOMMUNICATION INFORMATION:
TELEPHONE: (115) 705-8410
                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: de Boer, Piet A.J.
APPLICANT: Hale, Cynthia A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SCREENING
TITLE OF INVENTION: ANTIMICROBIALS
                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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CITY: Sa
STATE: C
COUNTRY:
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                                                                                                                                                                                                                                                NAME: Carroll, Peter G. REGISTRATION NUMBER: 32,837
                                                                                                                                              TOPOLOGY:
                                                                                                                                                     STRANDEDNESS:
                                                                                  19;
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5. 5948889
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                                                                                                                         S3 AA; 6100 MW; 12869 CN;
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                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                            California
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2741 MW;
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Pred. No. 6.87e-02;
Wismatches 1;
                                                                                Score 146; DB 2; Le
Pred. No. 6.87e-02;
2; Mismatches 1;
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Best Local
Patent No. 5795721

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROSS S. Rabin, Sumedha Jayasena
APPLICANT: and Larry Gold
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC
TITLE OF INVENTION: ACID LIGANDS OF ICP4
                                                                                                Sequence 5, Application US/08591989
                                                                                                                                         XXXXXX
                                                                                                                                                           US-08-591-989-5
                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                     Sequence 5, Application US/08591989 Patent No. 5795721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2 Patent No.
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                                                                                                                                                                                                  _
                                                                                                                                                                                                                  1 MGHHHHHHHHHHSSGHIEG--RHM 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide FINCE 54 AA; 6237 MW;
                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                 MGHHHHHHHHHSSGHIDDDDKHM
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                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                    TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                         NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
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Similarity 79.2%;
19; Conservet:
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                                                                                                                                                                                                                                                                                                                           54 amino acids
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Hale, Cynthia A.
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                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                          not relevant
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Pred. No. 6.87e-02;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                         y Match 4.18;
Local Similarity 79.28;
                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5
MEDIUM TYPE: storage
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,739
                                                                                                                                                                                          APPLICANT: Wolf, Marcia K.
APPLICANT: Cassels, Frederick J.
APPLICANT: Bell, Brian A.
                                                                                                                                                            TITLE OF INVENTION: Improved Methods for Production of TITLE OF INVENTION: Antigens Under Control of Temparture-Regulated NUMBER OF SEQUENCES: 5
                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                        STATE: V
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CITY: F
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STATE: Col-
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STREET: 8
                                                                                                                 ADDRESSEE: Glenna .....
correct: 9669 A Main Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
NCE 323 AA; 33944 MW; 442207 CN;
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Pred. No. 6.87e-02;
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Best Local Similarity 23.5%;
Matches 40; Conservative
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                                                                                                                                                                                                                                                                                                                                           XXXXXX
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                                                                                                                                                                                                                                                                       Sequence 2, Application PC/TUS9507748A
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                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLKIKYLLIGLSLSAMSSYSLAAAGPTLTKELALNVLSPAALDATWAPQDNLTLSNTG-V
ATTORNEY/AGENT INFORMATION:
NAME: HAILE, Ph.D., LISA
REGISTRATION NUMBER: 38,
                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                            APPLICANT: The Rege
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
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LENGTH: 168 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 425-4250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Hendricks, Glenna
                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                   FILING DATE: 1 CLASSIFICATION:
                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                         CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                    ADDRESSEE: Fish & Richardson .... STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: un
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                                                        APPLICATION NUMBER:
                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NISM: Cs3 protein
168 AA; 17464 MW; 155638 CN;
                                                                                                                                     92037
                                                                                                                                                USA
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                                                                                                                                                                                                                                     The Regents of the University of California ENTION: CLONED Borrelia burgdorferi VIRULENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
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V: 514
                                            16-JUN-1995
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            LISA A
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Pred. No. 1.82e+00;
48; Mismatches 72;
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                                                                              Version
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Best Local
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5099
INFORMATION: 908 520 ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-719-124-2
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                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Champion, Cheryl I
APPLICANT: Lovett, Michael A.
APPLICANT: Haake, David A.
APPLICANT: Miller, James N.
APPLICANT: Blanco, David R.
TITLE OF INVENTION: CLONED BO
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                         TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 3.0%;
Local Similarity 34.5%;
nes 20; Conservative
                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/719,124
FILING DATE: 24-SEP-1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                   STREET: 1000
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
JENCE 174 AA; 20290 MW; 153533 CN;
                                  SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
                                                                                           REFERENCE/DOCKET NUMBER: PD TELECOMMUNICATION INFORMATION:
                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/26
FILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
           *TOPOLOGY:
                     TYPE: amino acid
                                                                                                                     NAME: TUMARKIN, LISA A. REGISTRATION NUMBER: P-38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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1880 Century Park East, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lovett, Michael A.
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            linear
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12; Mismatches
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Pred. No. 1.87e+01
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                                            Query Match 3.0%;
Best Local Similarity 34.5%;
Matches 20; Conservative
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                       115 IKGYPNSIFDYLIQLDSDK-IDYAEKYGE-KARENFEESYKKDKITAVKQILKQILAD 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 LTGHGSSVLEELVQLVKDKNIDISIKYDPRKDSEVFANRVITDDIELLKKILAYFLPE 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08261825 Patent No. 5558993
 219 LTGHGSSVLEELVQLVKDKNIDISIKYDPRKDSEVFANRVITDDIELLKKILAYFLPE 276
                                                                                                                                                    TELEFAX: (619) 455-5110 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)_455-5100
                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: TUMARKIN, LISA A.
REGISTRATION NUMBER: P-31
                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 17-JUN-199
CLASSIFICATION: 435
                                                                                             MOLECULE TYPE: protein
JENCE 174 AA; 20290 MW; 153533 CN;
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                LENGTH:
TYPE: a
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CITY: Los Angeles
                                                                                                                     TOPOLOGY:
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Similarity 34.5%;
20; Conservative
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                                                        Score 106; DB 1;
Pred. No. 1.87e+01
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Pred. No. 1.87e+01;
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Suite 500
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RESULT ID US

US-08-328-254-6

STANDARD;

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Best Local Similarity 18.5%;
Matches 74; Conservative
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                                                                                                                  1673 KLRARLEADEKKQLCVLQQLKESEHHADLLKGRVENLERELEIARTNQEHAALEAENSKG
                                                                                                                                                                                                                                                                                                        1498 ADEKKOLHIAEKLKERE-REND-SLKDKVENL-ERELOMSEENQELVILDAENSKAEVET 1554
1790 LQEKEQEKVQMKEKSSTAMEMLQTQLKELNERVAALHNDQEACK-AKEQN-LSS-QVECL 1846
                                                                                                                                                                                                                                            1555 LKTQIEEMARSLKVFELDLVTLRSEKENLTKQIQE-KQGQLSELDK-LLSSFKSLLEEKE 1612
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                                                                                                                                                                                                               180 GKY-TDAVTVTVSNQEFMIRAYEQNPQHFIEDLEKVRVEQLTGHGSSVLEELVQLVKDKN
                                                                                                                                                 239 -IDISIKYDPRKDSEVFANRV--ITDDIELLKKILAYFLPEDTILKGG-HYDNQLQNGIK 294
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141
FILING DATE: 22-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P.C.
TELECOMMUNICATION INFORMATION:
TELECHHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 2482 amino acids
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APPLICATION NUMBER: US,
FILING DATE: 24-OCT-19
CLASSIFICATION: 435
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                                                         EVETLKA--KIEGMTQSLRGLELDVVTIRSEKENLTNELQKEQERISELEIINSSFE-NI 1789
                                                                                         RVKEFLESSPNTQW-ELRAFMAVMHFS-LTADRIDD-DI-LKVIVDSMNHHGDARSKLRE 350
                                                                                                                                                                                 QAEIQIKEESKTAVEMLQNQLKELNEAVAALCGDQEIMKATEQSLDPPIEEEHQLRNSIE 1672
                            ELAELTAELKIYSVIQAEINKHLSSSGTINIHDKSINLMDKNLYGYTDEEIFKASAEYKI
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Best Local :
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SEQUENCE 3248
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2341 QAEIQIKEESKTAVEMLQNQLKELNEAVAALCGDQEIMKATEQSLDPPIEEEHQLRNSIE 2400
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                                                    180 GKY-TDAVTVTVSNQEFMIRAYEQNPQHFIEDLEKVRVEQLTGHGSSVLEELVQLVKDKN 238
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                                                                                                                                                                                                                                                               7 Match 3.0%;
Local Similarity 18.4%;
nes 69; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-TOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/1621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR DEFENDED IN ORDER OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 36,25;
TELECOMMUNICATION INFORMATION
TELEPHONE: (215) 563-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Rattner, Jerome B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 3248 amino aci
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                                                                                                     LKTQIEEMARSLKIFELDLVTLRSEKENLTKQIQE-KQGQLSELDK-LLSSFKSLLEEKE 2340
                                                                                                                                                          SQDGNNHQFTTKVIGKDSRDFDISPKVNGENLVGDDVVLATGSQDFFVRSIGSKGGKLAA 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1601 Marke CITY: Philadelphia
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19103-2307
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Pred. No. 2.14e+01;
                                                                                                                                                                                                                                                                  Mismatches 171;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                               REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                   ANTI-SENSE: NO ORIGINAL SOURCE:
                             MOLECULE N
HYPOTHETICAL: N
                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                     SEQUENCE CHARACTERISTICS:
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CITY: F
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ZIP: 19103-2307
                                                                                                                                                          NAME: REED, JANET E. REGISTRATION NUMBER:
                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 09-DE
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                                                                       STRANDEDNESS:
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           ORGANISM:
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 3248 AA; 372207 MW;
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RATTNER, JEROME B.

IVENTION: MUCLEIC ACID ENCODING A

VENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN,

VENTION: AND METHODS OF USE
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S-DKSRPLNDLVSQK
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                                  ELEKAQLLQGLDEAK 2589
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                                                                     LEKMPQTTIQV-DGSEKKIVSIKDFLGSENKRTGALGNLKNSYSYNKDNNELSHFATTC-
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Similarity 18.4%;
69; Conservative
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Pred. No. 2.14e+01;
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Search completed: Sat Nov 27 15:37:44 1999 Job time: 27 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_nn n.a. n.a. database search, using Smith-Waterman algorithm

Fri Apr 25 18:54:05 1997; MasPar time 140.57 Seconds 971.672 Million cell updates/sec

Tabular output not generated

(1-1566) from US08699716A.seq >US-08-699-716A-1

Description:
Perfect Score:
N.A. Sequence: 1 ATGGGCCATCATCATCA......ATGACACGTCTGGTAAATGA
TACCCGGTAGTAGTAGTAGT.....TACTGTGCAGACCATTTACT

1566

Scoring table: TABLE Gap 6 default

Nmatch STD Dbase 0; Query 0

113505 seqs, 43611913 bases x

Post-processing: Minimum Match Listing first 4.0 summaries

Database:

n-geneseq25
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22

Statistics: Mean 9.447; Variance 5.762; scale 1.639

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	00 0		Result
3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	• • •	976 972 516 451 449	Score
22222 22222 22440	223.4	62.3 62.1 33.0 28.8 28.7	Query Match 1
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Human RPTP-beta.	5		Human gene signature	Generic DNA sequence	Generic DNA sequence	MCPC 603 VH CDR2 walk	Mixed oligonucleotide		pET-15b expression cl	Plasmid pET15b His-Ta	Human/mouse guanylate	Carbamoyl-phosphate-s	Sequence of a gene fr	Sequence encoding Cry	5' flanking region of	Type A insertion gene	Human brain Expressed	Generic DNA sequence	Generic DNA sequence	Generic DNA sequence	Mixed oligonucleotide	Ballast Constituent c	Generic DNA sequence	Generic DNA sequence	Generic DNA sequence	Generic DNA sequence	egiet to bive seducine
4.31e-02	4.31e-02	4.31e-02	1.31e-01	1.31e-01	4.31e-02		4.31e-02	4.31e-02	1.39e-02	1.39e-02	1.39e-02	1.39e-03	4.44e-03	4.44e-03	4.44e-03	4.44e-03	1.39e-03	1.39e-03	1.39e-03	1.39e-03		1.39e-03	4.28e-04	4.28e-04	1.30e-04	1.30e-04	3.90E-03

ALIGNMENTS

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RESULT COOL SOLUTION OF THE STATE OF OF TH
                                                                                                                                                           PT Recombinant DNA expressing Yersinia pestis V antigen - useful in protection and in parenteral vaccines for protection against plague claim 6; Page 11-13; Z5pp; English.

Claim 6; Page 11-13; Z5pp; English.

CC T04222-23 are DNA sequences (lcrV) encoding all or a protective epitopic part of the mature V protein of Versinia pestis. The protein was expressed as a fusion protein with maltose binding protein or capitathione- S-transferase in 3 different plasmid vectors. Y pestis is the highly virulent causative organism of plague in a wide range of animals, including man. The V antigen (LcrV) is an unstable 37.3 kDa monomeric peptide encoded on the ca. 70 kb Lcr plasmid. The V antigen is postulated to act as a virulence antigen, and transformed microorganisms contg. recombinant DNA encoding a V antigen protein/ peptide are useful in vaccines to protect against plague.

Sequence 1014 BP; 346 A; 181 C; 201 G; 286 T;
                                               Query Match
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T04222;
18-APR-1996 (first entry)
Partial LcrV (V antigen) gene of Y.
LcrV; V antigen; virulence; plague;
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Leary SEC, Titball RW, Wi
WPI; 95-328268/42.
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06-MAR-1995; G00481.
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T04223 standard; DNG.,
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T 18-APR-1996 (first entry)
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KW LCTV; V antigen; virulence;
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               plague;
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                pestis. vaccine;
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PC Claim 6; Page 15-16; 25pp; English.

CC PATC 101 PT DNA sequences (lorv) encoding all or a protective epitopic rolls of the mature V protein of Yersinia pestis. The protein was CC expressed as a fusion protein with maltose binding protein or CC glutathione- S-transferase in 3 different plasmid vectors. Y. pestis is the highly virulent causative organism of plague in a wide range of CC animals, including man. The V antigen (LcrV) is an unstable 37.3 kDa CC monomeric peptide encoded on the ca. 70 kb Lcr plasmid. The V antigen CC is postulated to act as a virulence antigen, and transformed CC microorganisms contg. recombinant DNA encoding a V antigen protein/ CC peptide are useful in vaccines to protect against plague.

SQ Sequence 1014 BP; 343 A; 185 C; 204 G; 282 T;
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                                                                                                                                 DNA constructs capable of transforming microorganisms - which can be grainst Yersinia pestis, at mucosal surfaces. Disclosure; Page 19-20; 27pp; English.
The sequence represents the plasmid pFORFIb including the entire Y. pestis cafl (F1) antigen gene having a 5' tail including a SacI (T page 19-20; and up to TATRA downstream of the cafl ORF.
The sequence represents the plasmid pFORFIb including a SacI (T page 19-20; and up to TATRA downstream of the cafl ORF.
The DNA construct can be used to transform human or animal gut (C colonizing microorganisms, specifically attenuated Salmonella (Typhimurium or Salmonella typhi. The transformed microorganisms (C can be used as live/attenuated vaccines which induce immune responses at mucosal surfaces. The vaccines provide protection (C against infection with Y. pestis, and are parenterally and orally active vaccines offering protection against bubonic and pneumonic (C plague vaccines offering protection against bubonic and pneumonic (C plague vaccines offering protection against bubonic and pneumonic (C plague vaccines offering protection against bubonic and pneumonic (C plague vaccines offering protection against bubonic and pneumonic (C plague vaccines offering protection against bubonic and pneumonic (C plague vaccines offering protection against bubonic and pneumonic (C plague vaccines offering protection against bubonic and pneumonic (C plague vaccines offering protection against bubonic and pneumonic (C plague vaccines offering protection against bubonic and pneumonic (C plague vaccines offering protection against bubonic and pneumonic (C plague vaccines offering protection against bubonic and pneumonic (C plague vaccines offering protection against bubonic and pneumonic (C plague vaccines offering protection against bubonic and pneumonic (C plague vaccines protection against bubonic and pneumonic (C plague vaccines page vaccines protection against bubonic and pneumonic (C plague vaccines page vaccines page vaccines page vaccines vaccines page vaccines page vaccine
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Vaccine; antigen; Salmonella typhimurium;
bubonic plaque; pneumonic plague; pneumonic plague;
DNA constructs capable of transforming microorganisms - which used as live or attenuated vaccines which induce an immune res against Yersinia pestis, at mucosal surfaces. Claim 7; Page 15-16; 27pp; English.

The sequence represents the plasmid pFGAL2a construct showing fusion of the first few bases of beta-galactosidase in the vector that the Y. pestis caf1 (F1) antigen minus its signal sequence having a 5' tail including a SacI restriction site, and up to caf1 AACC-3' end with some vector bases. The DNA construct ca
                                                                                                                                                                                                                                                                                                                                                           LT 4
Q92817
                                                                                                          23-DEC-1994; G02818.

24-DEC-1993; GB-026425.

(MINA) UK SEC FOR DEFENCE.

Howells A, Leary SEC, Oyston

WPI: 95-246396/32.
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misc_feature
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DNA constructs capable
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Best Loc
Matches
                                                         23-DEC-1994; G02818.
24-DEC-1993; GB-026425.
(MINA) UK SEC FOR DEFENCE.
Howells A, Leary SEC, Oyst
WPI; 95-246396/32.
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Yersinia pestis caf1 (F1) antigen in plasm
Vaccine; antigen; Salmonella typhimurium;
bubonic plague; pneumonic plague; ds.
Yersinia pestis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q92818 standa
Q92818;
17-DEC-1995
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Sequence 541 BP; 163 A; 120 C; 111 G; 147 T;
    used
                                                                                                                                                                                                                                                                                                       /*tag= a
misc_feature
                       DNA
                                          P-PSDB; R76527.
                                                                                                                                                                                                                                                    misc_feature
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The sequence represents the plasmid pFSIG3a construct showing the fusion of the first few bases of the E. coli LTB signal sequence with the Y. pestis caf1 (F1) antigen minus its signal sequence and having a 5' tail including a SacI restriction site, and up to the caf1 AACC-3' end with some vector bases. The DNA construct can be used to transform human or animal gut colonizing microorganisms, specifically attenuated Salmonella typhinurium or Salmonella typhic The transformed microorganisms can be used as live/attenuated vaccines which induce immune responses at mucosal surfaces. The vaccines which induce immune responses at mucosal surfaces. The vaccines provide protection against infection with Y. pestis, and are parenterally and orally active vaccines offering protection against bubonic and pneumonic plague.

Sequence 542 BP; 163 A; 122 C; 110 G; 147 T;
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Domain
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Q10572;
Q9-APR-1991 (fi
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Human Natriuretic Peptide Receptor B
NPRB; ANP; BNP; CNP; kidney failure;
/label= transmembrane
Domain
/label= cytoplasmic dc
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Disclosure; Page 17-18;
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Matches 8
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23-JUN-1989; US-370673.
(GETH ) GENENTECH INC.
Chang M, Goeddel D, Lowe
WPI; 91-036711/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1; 49pp; English.
The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having guanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the produc of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated MPRB of the protein has a mol wt. of 115 kD (calculated MPRB of the protein has a mol wt. of 115 kD (calculated MPRB of the protein for variants) can be used in treatment of natriuretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can
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Modified -site 600..602
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Modified -site 161..163
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d -site 277..279
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d -site 244..246
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d -site 195..197
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d -site 35..37
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larity 8.9%;
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atches 628;
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                                                                                                                                                        Query Match
Best Local
                                                                                                                               Matches
                                                                                                                                                                                                                                           Method for conducting gene therapy - comprises using recombinant gene encoding antibody binding antigen associated with a disease; useful for providing cell immunity.

Example 4; Page 23; 62pp; English.

The sequence given in Q81500 encodes an sFv anti-rev antibody consisting of the variable domains of the heavy and light chains of a mouse MAb against HIV-1 IIIB rev. The sFv specifically binds a highly conserved Rev domain. HeLa 74 cells expressing the SFV were resistant to all HIV-1 Clinical isolates tested.

Sequence 861 BP; 199 A; 234 C; 230 G; 198 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    set anti-rev sequence.

set anti-rev sequence.

HIV-1; human immunodeficiency virus type 1; AIDS; Rev protein; intracellular immunization; gene therapy; single chain antibody; intracellular immunization; resistance; cell immunity; HeLa; ss.
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WPI; 95-082039/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-FEB-1995.
28-JUL-1994; U08448.
30-JUL-1993; US-099870.
(UYJE-) UNIV JEFERSON
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AACCGGGGCGTTGGGTAATCTGAAAAACTCATACTCTTATA
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                                                                                                                               Similarity 70; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pomerantz
                                                                                                                        4.3%;
larity 97.2%;
Conservative
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                                                                                                                        Score 68; DB 14; L
Pred. No. 1.40e-25;
0; Mismatches 2;
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61

GACAAGCATATG gacaaccatatg

72 72

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                                              Query Ma
Best Loc
Matches
                                                                                                               Natriuretic protein receptor B - for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1; 49pp; English.

The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having guanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the produc. of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr-114,952). The protein (or variants) can be used in treatment of natriuretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q10572 standard; DNA; 1047
 1096
                                                                                                           also
                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC. Chang M, Goeddel D, Lowe WPI; 91-036711/05.
                                                                                                                                                                                                                                                         N-PSDB; Q10324.
                                                                                                                                                                                                                                                                                                                                                                                                                 /label= N-glycos_site
Modified -site 277..279
                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= N-glycc
Modified -site
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label N-glycos site
Modified -site 195..197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- N-glycos_site
Modified -site 161..163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Natriuretic Peptide Receptor B.
NPRB; ANP; BNP; CNP; kidney failure; heart fa
hyperaldosteronism; glaucoma; guanyl cyclase.
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23-JUN-1989; US-370673.
                                                                                                                                                                                                                                                                                                                                                                                         /label= N-glyco
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Modified -site 35..37
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/label= extracellular domain
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                                                                                                                                                                                                                                                                                                                                                                               label-
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GAATAACTGAATAAATCTTTAATTCGGCGG-TAAGCTCAGCTAATTCTTCACGCAACTTG
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                                                                                            prepd.
e 1047 BP;
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d -site 600..602
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d -site 349..?
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d -site 244..246
                                               Similarity
84; Conse
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                                              4.2%;
larity 8.3%;
Conservative
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274; 1
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Pred. No.
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                                               Mismatches
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                                                                       DB 2;
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1038
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RESULT TO AC TO DT OT OT KW TO KW CO

T29246

standard;

DNA;

1402 ВP

T29246;
07-JUL-1996 (first entry)
Type A neurotoxin C fragment-polyhistidine tag gene fusion.
Toxin; neurotoxin; fusion protein; antitoxin; vaccine; immu
Clostridium botulinum; polyhistidine; vector; pETHisa; pHis

vector; pETHisa; pHisBot;

immunogen;

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                                                                         TATGTAAGAGTGATGCGGGCTGGTTCAACAAGAGTTGCCGTTGCAGTGGTGCTTGCAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 10
NB1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                affinity tag and respect to the phisbot process are botulinum type A neurotoxin. The phisbot process are purified by in Escherichia coli as a soluble protein and was purified by metal chelate affinity chromatography to obtain a product from metal chelate affinity chromatography to obtain a product from the phisbot process are product from the phisbot process.
Random point mutations were introduced into the alpha fragment E.coli beta-galactosidase. The wild type sequence was obtained single stranded template and an oligonucleotide was hybridised it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can amplified and then expressed in a suitable host-vector system.
                                                                                                                                                                                                 misincorporation, completion
Disclosure; p; English.
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                                                                                                                                                                                                                                                                                        (SUSO) SUOMEN SOKERI OY. Lehtovaara P, Knowles J, WPI; 88-279927/40.
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03-APR-1987; US-034819.
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                                                                                                                                                                                                                                                                                                                                                                                                   EP-285123-A.
05-MAY-1988.
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EP-285123-A.
05-MAY-1988; 105163.
30-MAY-1988; 105163.
03-APR-1987; US-034819.
(SUSO) SUOMER SOKERI OY.
Lehtovaara P, Knowles J,
WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence covers a occurred singularly: See also P80575.
Sequence 204 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cross reacted to a few non-mycobacterial infection. be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59. Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
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01-DEC-1993.
24-MAY-1993;
26-MAY-1992;
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Q51746
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Shank DD, Spears
WPI; 93-378844/48
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Oligonucleotide
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/*tag= b
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tuted E.coli beta-galactosidase
galactosidase alpha-fragment; b
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probe MK14-A
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1.71e-09;
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Best Local S
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Matches 0; Conse
                                                                                  Q70467
05-APR-1995 (first entry)
05-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
affactor domain; concateneated heterofunctional protein; linker;
                                                                                                                                                                                                                                                                                                                                                        WPI; 93-3/66447...
New oligo:nucleotide probes
Assection and amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-1993.
24-MAY-1993;
26-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Introducing : by prepn of
                                                                                                                                                                                                                                                  Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                       26-r..
(BECT ) be.
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Q51746;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAY-1994 (fi
Oligonucleotide |
Oligonucleotide;
                                                                     Q70467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       occurred singularly in any See also P80575. Sequence 204 BP; 21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transcriptase and the molecules are completed to forms that can amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of where the sequence covers are substitutions.
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                                                                                     standard;
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de probe MK14-A
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of Mycobacteria nucleic acio
                                                                                                                                                                                                               Score 38; DB 9; I
Pred. No. 7.93e-08;
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Pred. No. 1.71e-09;
53; Mismatches 39
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PS Disclosure; Page 35; 255pp; English.

CC Q70467 is a generic DNA sequence used to generate random TSAR (Totally

CC Synthetic Affinity Reagents) peptides. This generic formula can also be

CC represented as follows: X(NNB)16(TGC)(NNB)12(NNB)16(TGC)(NNB)11. X

CC and y are flanking restriction sites (X is not the same as Y) that are

CC ont specific peptides generated by these generic sequences are shown in

CC (Ther specific peptides generated by these generic sequences are shown in

CC (Ther specific peptides generated by these generic sequences are shown in

CC (Ther specific peptides generated by these generic sequences are shown in

CC (Ther specific peptides generated by these generic sequences are shown in

CC (Ther specific peptides accord effector peptide portion that is

CC (Ther specific peptide and a second effector peptide portion that is

CC (Ther specific peptide contains. The oligonucleotides are also designed so

CC (Ther specific peptide contains 2 or 4 cysteine residues positioned

CC (Ther some degree of conformational rigidity to the peptides. The TSARS

CC (Ther some degree of conformational rigidity to the peptides. The TSARS

CC (Ther specific peptide, toxin or enzyme, to the specific target or on the

CC (Ther specific target or on the function of macromolecules, eg.
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Best Local
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Q70469 standard;
Q70469;
Q7-APR-1995 (fir
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Fowlkes DM, Kay BK;
WPI; 94-279739/34.
P-PSDB; R65153.
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01-FEB-1994; U00977.

01-FEB-1993; US-013416.

30-DEC-1993; US-176500.

31-JAN-1994; US-189331.
/note= "this sequence
sequence of 6,9 or 12
                                                                                                                                                       Generic DNA sequence to generate a random TSAR peptide 1: TSAR; totally synthetic affinity reagent; synthetic; bind effector domain; concateneated heterofunctional protein; direct; rapid; detection; screening; treatment; generic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           monoclonal or polyclonal antibodies and therefore circumvent the need complex methods of hybridoma formation or in vivo antibody production The TSARs are easily characterised and have designed activity allowing the teachers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       direct
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                                                                             misc_feature
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                                                                                                                                      Synthetic.
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                                                                             Location/Qualifiers 55..60
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represents 'Z'; nucleotides (see
                                                                                                                                                                                                                                                                                                                                   BP.
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2 C; 2 G; 2 T;
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33; M
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                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                              Query Match
Best Local
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWlkes DM, Kay EK;
WPI; 94-279739/34.
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W09418318-A.
18-AUG-1994.
                                                                                                                                                                                                                                                                                                                         detection in a screening process. Sequence 114 BP; 0 A; 4 C;
                                                                                                                                                                                                                                                                                                                                                                        characterised and have designed activity allowing direct and rapid
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169 GAGTTGCCGTTGCAGTGGTGCTTGCAGTTAAATCTGCCGCATTAGCAGTTGC 118
                                                                                                      229 CCATAATTGTAATTGGAGCGCCTTCCTTATATGTAAGAGTGATGCGGGCTGGTTCAACAA 170
                                                                                                                                                                                                                y Match 2.3%;
Local Similarity 8.0%;
hes 9; Conservative
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                                                    Score 36; DB 12; Le
Pred. No. 9.77e-07;
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